

STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 155185

TO: Emily M Le
Location: 3c35/3c18
Art Unit: 1648
Friday, June 03, 2005

From: Noble Jarrell
Location: Biotech-Chem Library
Rem 1B71
Phone: 272-2556

Case Serial Number: 08/869386

Noble.jarrell@uspto.gov

Search Notes

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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CRFE 155183

Jarrell, Noble

From: Le, Emily
Sent: Wednesday, June 01, 2005 6:34 PM
To: Jarrell, Noble
Subject: FW: Sequence Search: 08869386

Hi Noble,

I noted a discrepancy in an amino acid residue present in SEQ ID NO: 3. Thus, please provide another search for seq id no:3 ,wherein the sequence is: NNTRKSIRIQRGPGRAFVTIGKIG.

Thanks, Noble!!

-----Original Message-----

From: Le, Emily
Sent: Monday, May 16, 2005 12:04 PM
To: Jarrell, Noble
Subject: FW: Sequence Search: 08869386

update:

Please provide a search for the following:

1. RAFVTIGK, which is SEQ ID NO: 5 in the above case.
2. SEQ ID NO: 1
3. SEQ ID NO: 3

Please also limit the size to no more than 25 amino acids.

Thanks, Noble.

Emily

-----Original Message-----

From: Le, Emily
Sent: Friday, May 13, 2005 4:13 PM
To: Jarrell, Noble
Subject: Sequence Search: 08869386

Noble,

Please provide a search for the following:

1. RAFVTIGK

Please also limit the size to no more than 25 amino acids.

Thanks!

Emily Le

Noble
Done 6/13/05
2 AFA
Compare 1/16
10 prep
10 cond

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 3, 2005, 03:11:57 ; Search time 38 Seconds
(without alignments)
60.768 Million cell updates/sec

Title: SEQ1
Perfect score: 122.11111111111111
Sequence: 1 Mntfkrkfrtdrgpgrafvtgikg 24

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 4989

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 250 summaries

Database : PIR 79:.*
1: piri:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	64	52.5	20	2 S65399	immunodeficiency v
2	29	23.8	17	2 S66213	Glucose 1-dehydrog
3	27	22.1	20	2 S48654	Plasmeprin II - ma
4	26.5	21.7	14	2 PA0109	porin por 1B - Ara
5	26.5	21.7	14	2 PA0045	porin por1 - Arabi
6	26	21.3	13	2 S03879	6-phosphofructokin
7	25	20.5	10	2 D28027	protein P7 - curle
8	25	20.5	12	2 S11286	exo-alpha-sialidas
9	25	20.5	16	2 JN0264	translation initia
10	24.5	20.1	17	2 A37823	dihydroliipoamide S
11	24	19.7	7	2 PT0515	T-cell receptor be
12	24	19.7	13	2 C53275	Ig kappa-1 chain J
13	24	19.7	14	2 PH0915	T-cell receptor be
14	24	19.7	20	2 S63490	dissimilatory sulf
15	24	19.7	21	2 S31427	biliary glycoprote
16	24	19.7	22	2 C42856	hypothetical prote
17	24	19.7	24	2 S21511	incFVI protein - E
18	24	19.7	25	2 D41575	bombinin-like pept
19	23.5	19.3	22	2 A28524	diaminopropionate
20	23	18.9	10	2 S65388	cytochrome-c oxida
21	23	18.9	15	2 PH0797	T-cell receptor al
22	23	18.9	17	2 I51203	myosin heavy chain
23	23	18.9	17	2 AP2093	heterocyst-inhibit
24	23	18.9	18	2 S39153	translation elonga
25	23	18.9	19	2 I49037	TcR Delta chain V-
26	23	18.9	20	2 B53592	Hx-exporting Atpas
27	23	18.9	24	2 C47689	flagellar core pro
28	23	18.9	25	2 B47689	flagellar core pro
29	22	18.0	12	2 S65629	protoporphyrinogen

30	22	18.0	20	2 S03505	T-cell receptor al
31	22	18.0	20	2 S31220	B2x protein - bovi
32	22	18.0	20	2 B47642	T-cell surface gly
33	22	18.0	20	2 DIRT	dermatan fluid tra
34	22	18.0	21	2 A60225	pyruvate dehydrog
35	22	18.0	22	2 PQ0070	T-cell receptor be
36	22	18.0	22	2 B90996	probable transcrip
37	22	18.0	23	2 S47192	T-cell receptor J-
38	22	18.0	23	2 G69812	hypothetical prote
39	22	18.0	24	2 D27579	T-cell receptor be
40	22	18.0	25	1 ZJBPG4	gene J protein - p
41	22	18.0	25	2 S62673	glyceroldehyde-3-p
42	22	18.0	25	2 S22221	peroxidase (EC 1.1
43	22	18.0	25	2 S10850	alpha-amylase inhi
44	21	17.2	10	2 S77990	cytochrome-c oxida
45	21	17.2	13	2 S33800	chaperone, TCP1-re
46	21	17.2	14	2 PH1347	Ig heavy chain DJ
47	21	17.2	16	2 H41299	T-cell receptor al
48	21	17.2	16	2 A42411	myosin light chain
49	21	17.2	16	2 I51879	cystathionine beta
50	21	17.2	18	2 S09722	2S albumin small c
51	21	17.2	21	2 I50535	calmodulin - elect
52	21	17.2	22	2 A39269	LX-1 tumor antigen
53	21	17.2	23	2 S43765	ribosomal protein
54	21	17.2	24	4 T01780	probable gag polym
55	21	17.2	25	2 S51071	ribosomal protein
56	21	17.2	25	2 B69274	hypothetical prote
57	21	17.2	25	2 S65729	hemoglobin, extrac
58	20.5	16.8	18	2 A25941	Ig heavy chain J-H
59	20.5	16.8	24	2 D53402	glTX 5'-region con
60	20	16.4	9	4 I73804	hypothetical E2 pr
61	20	16.4	11	2 S13279	lie-Ser-bradykinin
62	20	16.4	15	2 S43634	cytochrome-c oxida
63	20	16.4	15	2 S57577	T cell receptor V-
64	20	16.4	15	2 D28587	T-cell receptor be
65	20	16.4	15	2 C34874	transforming prote
66	20	16.4	16	2 PH1790	T cell receptor al
67	20	16.4	16	2 PH1771	T cell receptor al
68	20	16.4	16	2 C49048	T-cell receptor be
69	20	16.4	16	2 PH1580	Ig H chain V-D-J r
70	20	16.4	17	2 B61321	histone H4 - chick
71	20	16.4	17	2 A61321	histone H4 - commo
72	20	16.4	18	2 PQ0072	T-cell receptor be
73	20	16.4	18	2 S28396	T-complex protein
74	20	16.4	19	2 S28396	CAMP-regulated pho
75	20	16.4	20	1 LFBSTT	tet leader peptide
76	20	16.4	20	2 A36016	granulocyte inhibi
77	20	16.4	20	2 A61264	MHC class I histoc
78	20	16.4	20	2 S68620	histone H4 - sea u
79	20	16.4	20	2 S65884	translation initia
80	20	16.4	20	2 S16478	tray protein - Esc
81	20	16.4	20	2 PS0188	superoxide dismuta
82	20	16.4	20	2 A42865	Ca2+/calmodulin-de
83	20	16.4	20	2 A42267	J-kappa recombinat
84	20	16.4	21	2 S47202	T-cell receptor J-
85	20	16.4	22	2 S47206	T-cell receptor be
86	20	16.4	22	2 S05590	T-cell receptor be
87	20	16.4	22	2 JC1488	hypothetical 2.5K
88	20	16.4	22	2 PC7072	Hx-transporting tw
89	20	16.4	23	2 S43289	cytochrome-c oxida
90	20	16.4	23	2 I51431	histone H4-1 precu
91	20	16.4	23	2 A47415	mannose-1-phosphat
92	20	16.4	24	2 B30609	Ig kappa chain V-I
93	20	16.4	24	2 B43295	histone H4 - alfa
94	20	16.4	24	2 A43941	extracellular mura
95	20	16.4	24	2 A37825	fibronectin recept
96	20	16.4	25	2 S43633	cytochrome-c oxida
97	20	16.4	25	2 PC1221	alanine racemase (
98	20	16.4	25	2 A60807	heat shock protein
99	20	16.4	25	2 A34179	neuromedin U - com
100	20	16.4	25	2 A60741	insulin-like growt
101	20	16.4	25	2 S36378	Ig heavy chain V r
102	20	16.4	25	2 S21197	hydrogensulfite re

103	20	16.4	25	2	A61457	alpha-glucosidase
104	19.5	16.0	15	2	F28587	T-cell receptor be
105	19.5	16.0	18	2	S03528	Ig heavy chain J1
106	19.5	16.0	20	2	A47687	3-dehydroquininate d
107	19	15.6	7	2	A33098	244K exoantigen -
108	19	15.6	9	2	A41978	calliFMRamide 5 -
109	19	15.6	9	2	B20569	serum amyloid P-co
110	19	15.6	10	2	F31345	Ig heavy chain DJ
111	19	15.6	11	2	C37196	bradykinin-potenti
112	19	15.6	11	2	D37196	collagen alpha 2(V
113	19	15.6	12	2	D46662	hypothetical prote
114	19	15.6	12	2	D28551	Ig kappa-1 chain J
115	19	15.6	12	2	C20907	Ig kappa-2 chain J
116	19	15.6	12	2	F20907	Ig kappa chain J s
117	19	15.6	13	2	S23640	alpha-2 collagen -
118	19	15.6	13	2	I50173	lutropin beta chai
119	19	15.6	14	2	B61309	alcohol dehydrogen
120	19	15.6	14	2	S11074	Ig heavy chain DJ
121	19	15.6	15	2	PH1342	T-cell receptor be
122	19	15.6	15	2	I53284	flt3 ligand isofo
123	19	15.6	15	2	I78838	H+-transporting tw
124	19	15.6	15	2	PT0091	chemoattractant pr
125	19	15.6	15	2	A36279	epidermal growth f
126	19	15.6	15	2	S08301	Ig heavy chain CDR
127	19	15.6	16	2	FT0224	T-cell receptor be
128	19	15.6	16	2	G49039	T-cell receptor be
129	19	15.6	16	2	B28587	T-cell receptor al
130	19	15.6	16	2	F53284	T-cell receptor al
131	19	15.6	16	2	PH1453	25K kidney and gal
132	19	15.6	16	2	E58501	protein kinase - h
133	19	15.6	16	2	I37452	ribosomal protein
134	19	15.6	16	2	S78415	ferredoxin-NADP re
135	19	15.6	16	2	A44897	hypothetical prote
136	19	15.6	16	4	A33171	T-cell receptor be
137	19	15.6	17	2	B49404	T-cell receptor be
138	19	15.6	17	2	D53284	photosystem II pro
139	19	15.6	17	2	S05033	T cell receptor be
140	19	15.6	18	2	I73024	T-cell receptor be
141	19	15.6	18	2	B40741	brain-associated s
142	19	15.6	18	2	A61392	Ig heavy chain DJ
143	19	15.6	18	2	PH1350	T-cell receptor be
144	19	15.6	18	2	A49404	alpha-macroglobuli
145	19	15.6	18	2	S70612	tubulin beta-3 cha
146	19	15.6	18	2	S60229	vitronectin - shee
147	19	15.6	19	2	S22233	tet leader peptide
148	19	15.6	20	1	LFBSU1	flavodoxin B - Azo
149	19	15.6	20	2	S17461	malate dehydrogena
150	19	15.6	20	2	S04961	crystallin - Pacif
151	19	15.6	20	2	B60894	tet leader peptide
152	19	15.6	20	2	S23742	hypothetical prote
153	19	15.6	20	2	S26748	T-cell receptor be
154	19	15.6	20	2	C49404	jacalin beta-1 cha
155	19	15.6	20	2	S29636	superoxide dismuta
156	19	15.6	20	2	P00732	lamin B receptor -
157	19	15.6	20	2	S28405	metalloproteinase
158	19	15.6	20	2	A58903	H+-transporting tw
159	19	15.6	20	2	B35473	T-cell receptor J-
160	19	15.6	21	2	S47205	sperm chromatin pr
161	19	15.6	21	2	PN0082	hypothetical 2.5K
162	19	15.6	21	2	JQ2196	Ig heavy chain DJ
163	19	15.6	21	2	PH1369	probable nitrate r
164	19	15.6	21	2	S61306	interleukin-7 rece
165	19	15.6	22	2	B40256	T-cell receptor J-
166	19	15.6	22	2	F47193	probable antigen 6
167	19	15.6	22	2	F41476	collagen alpha 3(I
168	19	15.6	22	2	S64675	L-serine dehydrata
169	19	15.6	22	2	S16224	translation initia
170	19	15.6	22	2	PT0052	hypothetical prote
171	19	15.6	22	2	F84018	T-cell receptor J-
172	19	15.6	23	2	S47191	T-cell receptor J-
173	19	15.6	23	2	S47210	T-cell receptor be
174	19	15.6	23	2	S07967	nucleoside-diphosp
175	19	15.6	24	2	S47563	

176	19	15.6	24	2	B60422	MSBL-neurophysain -
177	19	15.6	24	2	PH1916	T-cell receptor be
178	19	15.6	24	2	A53591	envelope protein g
179	19	15.6	24	2	UC4804	core protein J - p
180	19	15.6	24	2	S22333	gene J protein - p
181	19	15.6	24	2	PC2176	exo-alpha-sialidas
182	19	15.6	24	2	PH1336	Ig heavy chain DJ
183	19	15.6	24	2	T24611	hypothetical prote
184	19	15.6	25	2	S07574	malate dehydrogena
185	19	15.6	25	2	D26889	pancreatic endoppa
186	19	15.6	25	2	D26889	T-cell receptor be
187	19	15.6	25	2	F49533	T-cell receptor be
188	19	15.6	25	2	PH1354	Ig heavy chain DJ
189	18.5	15.2	23	2	B26091	leukocyte glycopro
190	18.5	15.2	25	2	C37520	glutathione transf
191	18	14.8	5	2	S35595	hypothetical prote
192	18	14.8	9	2	S39437	D-amino-acid oxida
193	18	14.8	9	2	B45020	probable minipolyp
194	18	14.8	9	4	E15595	orf 2 rara 5'-regi
195	18	14.8	10	1	EC1Q1M	tachykinin I - mig
196	18	14.8	10	2	S24190	tryptase (BC 3.4.2
197	18	14.8	10	2	A27617	triose-phosphate i
198	18	14.8	10	2	S26506	collagen alpha 1(V
199	18	14.8	11	2	S33300	probable substance
200	18	14.8	12	2	A56878	light yellow cell
201	18	14.8	13	2	PH0799	T-cell receptor al
202	18	14.8	14	2	PH1308	hemocyanin chain 3
203	18	14.8	14	2	PH1332	Ig heavy chain DJ
204	18	14.8	14	2	B28018	very late antigen-
205	18	14.8	14	2	PH0804	T-cell receptor al
206	18	14.8	14	2	S21308	hemocyanin chain 3
207	18	14.8	15	2	S21238	hydrogensulfite re
208	18	14.8	15	2	S13973	chlorophyll a/b-bi
209	18	14.8	15	2	PA0034	protein QA300024 -
210	18	14.8	15	2	A58970	GLYNA1 - soybean (
211	18	14.8	15	2	PA0106	protein_QF200076 -
212	18	14.8	15	2	A56963	acid phosphatase (
213	18	14.8	15	2	A28497	neurotensin-relate
214	18	14.8	15	2	JT0610	leukocyte chemoatt
215	18	14.8	16	2	H41425	cytochrome P450 IF
216	18	14.8	16	2	B29501	fibrinopeptide A -
217	18	14.8	16	2	S16376	L-serine dehydrata
218	18	14.8	16	2	A35552	caldesmon - turkey
219	18	14.8	17	2	S32587	L-ascorbate peroxi
220	18	14.8	17	2	PT0235	Ig heavy chain CRD
221	18	14.8	17	2	I24687	T-cell receptor be
222	18	14.8	17	2	A46592	lactase-philorizin
223	18	14.8	17	2	S61451	hypothetical prote
224	18	14.8	17	2	I67524	CD33 antigen homol
225	18	14.8	18	2	T08159	S locus-linked pro
226	18	14.8	18	2	A35678	hypothetical prote
227	18	14.8	19	2	I49422	L-lactate dehydrog
228	18	14.8	19	2	A41668	integrin alpha-7 c
229	18	14.8	19	2	PC1322	hypothetical prote
230	18	14.8	19	2	S63510	phosphonoacetaldeh
231	18	14.8	19	2	PC1324	hypothetical prote
232	18	14.8	20	2	A53875	creatine kinase (E
233	18	14.8	20	2	B34817	collagenolytic pro
234	18	14.8	20	2	C34817	collagenolytic pro
235	18	14.8	20	2	E39419	collagen alpha 5(I
236	18	14.8	20	2	A05332	serum amyloid p-co
237	18	14.8	20	2	PL0145	carbon-monoxide de
238	18	14.8	20	2	S28434	hypothetical prote
239	18	14.8	20	2	B30208	major outer membra
240	18	14.8	20	2	S28434	nikkomycin synthet
241	18	14.8	20	2	S53440	glutathione-bindin
242	18	14.8	20	2	S78759	ribosomal protein
243	18	14.8	20	2	A39543	collagen alpha 1(I
244	18	14.8	21	2	SL2055	glyceraldehyde-3-p
245	18	14.8	21	2	PT0089	4-hydroxybenzoate
246	18	14.8	21	2	S48632	carbanic anhydrase
247	18	14.8	21	2	A20359	translation elonga
248	18	14.8	21	2	C39543	collagen alpha 3(I

249 18 14.8 22 2 B60475 Glyceraldehyde-3-p
250 18 14.8 22 2 JN0911 N4-(beta-N-acetyl

ALIGNMENTS

RESULT 1
S65399
immunodeficiency virus type 1, HIV-1 gp120 - human (fragments)
C:Species: Homo sapiens (man)
C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C:Accession: S65399
R;Niwa, Y.; Yano, M.; Futaki, S.; Okumura, Y.; Kido, H.
Eur. J. Biochem. 237, 64-70, 1996
A>Title: T-cell membrane-associated serine protease, tryptase TL(2), binds human immunod
man immunodeficiency virus type 1 inhibit cleavage of gp120.
A:Reference number: S65399; MUID:96203909; PMID:8620895
A:Accession: S65399
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-10;11-20 <NIW>
C:Superfamily: type E retrovirus env polyprotein

Query Match 52.5%; Score 64; DB 2; Length 20;
Best Local Similarity 92.3%; Pred. No. 0.001;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 11 RGPGRFVTIGKI 23
Db 1 RGPGRFVTIGRI 13

RESULT 2
S66213
Glucose 1-dehydrogenase (EC 1.1.1.47) - Haloferax mediterranei (fragment)
C:Species: Haloferax mediterranei
C>Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S66213
R;Bonete, M.J.; Pire, C.; Llorca, F.I.; Camacho, M.L.
FEBS Lett. 383, 227-229, 1996
A>Title: Glucose dehydrogenase from the halophilic Archaeon Haloferax mediterranei: enzy
A:Reference number: S66213; MUID:96198607; PMID:8925901
A:Accession: S66213
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-17 <BON>
A:Cross-references: UNIPROT:Q977U7
C:Keywords: oxidoreductase

Query Match 23.8%; Score 29; DB 2; Length 17;
Best Local Similarity 42.9%; Pred. No. 4.2e+02;
Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 5 KSTRIQRGPGRFV 18
Db 2 KATAVKRGEDRPV 15

RESULT 3
S48654
Plasmepein II - malaria parasite (Plasmodium falciparum)
C:Species: Plasmodium falciparum
C>Date: 15-Jul-1995 #sequence_revision 19-Apr-1996 #text_change 09-Jun-2000
C:Accession: S48654
R;Hill, J.; Tyas, L.; Phylip, L.H.; Kay, J.; Dunn, B.M.; Berry, C.
FEBS Lett. 352, 155-158, 1994
A>Title: High level expression and characterisation of Plasmepein II, an aspartic prote
A:Reference number: S48654; MUID:95010698; PMID:7925966
A:Accession: S48654
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-20 <HIL>

Query Match 22.1%; Score 27; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 1e+03;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 10 QRGGRGFVTIG 21
Db 9 QMGRGSEHLTIG 20

RESULT 4
PA0109
porin por 1B - Arabidopsis thaliana (fragment)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 07-Apr-1995 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C:Accession: PA0109
R;Kamo, M.; Kawakami, T.; Tsugita, A.
submitted to JIPID, March 1995
A:Reference number: PA0109
A:Accession: PA0109
A:Molecule type: protein
A:Residues: 1-14 <KAM>
A:Cross-references: UNIPROT:Q8LA84; UNIPROT:Q42292
A:Experimental source: root

Query Match 21.7%; Score 26.5; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 8.9e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

Qy 11 RGPGRFVTIGK 22
Db 2 KGFG-LYTEIGK 12

RESULT 5
PA0045
porin por1 - Arabidopsis thaliana (fragment)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: PA0045
R;Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
submitted to JIPID, July 1994
A:Description: Separation and characterization of Arabidopsis proteins by two-dimensio
A:Reference number: PA0001
A:Accession: PA0045
A:Molecule type: protein
A:Residues: 1-14 <KAM>
A:Cross-references: UNIPROT:Q7M1W9
A:Experimental source: root

Query Match 21.7%; Score 26.5; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 8.9e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

Qy 11 RGPGRFVTIGK 22
Db 2 KGFG-LYTEIGK 12

RESULT 6
S03879
6-phosphofructokinase (EC 2.7.1.11) B - rabbit (fragment)
N;Alternate names: phosphofructo-1-kinase B
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C:Accession: S03879
R;Valaitis, A.P.; Foe, L.G.; Kwiatkowska, D.; Latashaw, S.P.; Kemp, R.G.
Biochim. Biophys. Acta 995, 187-194, 1989
A>Title: The sites of phosphorylation of rabbit brain phosphofructo-1-kinase by cyclic A
A:Reference number: S03878; MUID:89194250; PMID:2539199
A:Accession: S03879
A:Molecule type: protein
A:Residues: 1-13 <VAL>

A;Cross-references: UNIPROT:Q7M3P5

A;Note: the sequence from the summary is inconsistent with that from table I and Fig. 4

C;Keywords: glycolysis; phosphotransferase

Query Match 21.3%; Score 26; DB 2; Length 13;
Best Local Similarity 40.0%; Pred. No. 1e+03;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 TRKSIRIQRG 12

DB 3 TRRSLSMDKG 12

RESULT 7

D28027

protein P7 - curled-leaved tobacco (fragment)

C;Species: Nicotiana glauca (curled-leaved tobacco)

C;Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 09-Jul-2004

C;Accession: D28027

R;Bauw, G.; De Loose, M.; Inze, D.; Van Montagu, M.; Vandekerckhove, J.

Proc. Natl. Acad. Sci. U.S.A. 84, 4806-4810, 1987

A;Title: Alterations in the phenotype of plant cells studied by NH2-terminal amino acid-

A;Reference number: A94167

A;Accession: D28027

A;Molecule type: protein

A;Residues: 1-10 <BAU>

A;Cross-references: UNIPROT:Q7M1V8

Query Match 20.5%; Score 25; DB 2; Length 10;

Best Local Similarity 71.4%; Pred. No. 1.1e+03;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 14 GRAFVTI 20

DB 3 GRSEFVI 9

RESULT 8

S11286

exo-alpha-sialidase (EC 3.2.1.18) - influenza A virus (strain A/FPV/Rostock/34 [H7N1])

A;Alternate names: neuraminidase

C;Species: influenza A virus

C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 22-Jun-1999

C;Accession: S11286

R;Robertson, J.S.

Nucleic Acids Res. 6, 3745-3757, 1979

A;Title: 5' and 3' terminal nucleotide sequences of the RNA genome segments of influenza

A;Reference number: S11286; MUID:80034428; PMID:493121

A;Accession: S11286

A;Molecule type: genomic RNA

A;Residues: 1-12 <ROB>

A;Cross-references: EMBL:J02114; NID:G324483; PIDN:AAA43398.1; PID:G324486

C;Genetics:

A;Map position: segment 6

C;Superfamily: influenza virus exo-alpha-sialidase

C;Keywords: glycosidase; hydrolase

Query Match 20.5%; Score 25; DB 2; Length 12;

Best Local Similarity 44.4%; Pred. No. 1.3e+03;

Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 13 PGRAFVTIG 21

DB 3 FNQKIITIG 11

RESULT 9

JN0264

translation initiation factor eIF-2 gamma chain - pig (fragment)

N;Alternate names: eIF2 gamma chain

C;Species: Sus scrofa domestica (domestic pig)

C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 09-Jul-2004

C;Accession: JN0264

R;Mukoyama, E.B.; Shiohara, H.; Suzuki, H.

Biochem. Biotechnol. Biochem. 56, 680-681, 1992

A;Title: GTP-binding sequences in the gamma subunit of pig liver initiation factor 2.

A;Reference number: JN0264; MUID:92282179; PMID:1368212

A;Accession: JN0264

A;Molecule type: protein

A;Residues: 1-16 <MUK>

A;Cross-references: UNIPROT:Q9TRQ9

A;Experimental source: liver

C;Keywords: GTP binding

F;1-16/Region: GTP binding #status experimental

Query Match 20.5%; Score 25; DB 2; Length 16;

Best Local Similarity 50.0%; Pred. No. 1.8e+03;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 15 RAFVTICKIG 24

DB 1 QATINIGTIG 10

RESULT 10

A37823

dihydrolipoamide S-acetyltransferase (EC 2.3.1.12) - bovine (fragment)

C;Species: Bos primigenius taurus (cattle)

C;Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 09-Jul-2004

C;Accession: A37823

R;Rahmatullah, M.; Radke, G.A.; Andrews, P.C.; Roche, T.E.

J. Biol. Chem. 265, 14512-14517, 1990

A;Title: Changes in the core of the mammalian-pyruvate dehydrogenase complex upon select

A;Reference number: A37823; MUID:90354445; PMID:2167319

A;Accession: A37823

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-17 <RAH>

A;Cross-references: UNIPROT:Q7M2M8

C;Keywords: acyltransferase; coenzyme A

Query Match 20.1%; Score 24.5; DB 2; Length 17;

Best Local Similarity 66.7%; Pred. No. 2.3e+03;

Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 12 GP-GRFVT 19

DB 1 GPKGRVFVS 9

RESULT 11

PT0515

T-cell receptor beta chain V-D-J region (100-4AE) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C;Accession: PT0515

R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A;Reference number: PT0509; MUID:91277601; PMID:1711558

A;Accession: PT0515

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-7 <FEE>

A;Experimental source: adult thymus, strain BALB/c

C;Keywords: T-cell receptor

Query Match 19.7%; Score 24; DB 2; Length 7;

Best Local Similarity 80.0%; Pred. No. 2.8e+05;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 GPGRA 16

DB 3 GPGQA 7

RESULT 12

CS3275
Ig kappa-1 chain J3 segment b95 allotype - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 16-Aug-1996
C:Accession: CS3275

R:Ayadi, H.; Marche, P.N.; Cazenave, P.A.

Immunogenetics 34, 201-207, 1991

A:Title: Evolution of the rabbit immunoglobulin kappa chain genes.

A:Reference number: A53275; MUID:91372868; PMID:1909995

A:Accession: CS3275

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-13 <AYA>

A:Comment: This J3 segment may not be functional because of substitutions in the 7 mer a

C:Keywords: heterotetramer; immunoglobulin

Query Match 19.7%; Score 24; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 RGGP 14

Db 3 RGGP 6

RESULT 13

PH0915
T-cell receptor beta chain V-D-J region (isolate 1) - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C>Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997

C:Accession: PH0915

R:Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenberg, A.A.; Wilson, D.B.

J. Exp. Med. 174, 1467-1476, 1991

A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergy

A:Reference number: PH0891; MUID:92078857; PMID:1836012

A:Accession: PH0915

A:Molecule type: mRNA

A:Residues: 1-14 <GOL>

A:Experimental source: concanavalin A-activated lymphoblast

A>Note: the authors translated the codon GGG for residue 8 as Glu and GAG for residue 9

C:Keywords: T-cell receptor

Query Match 19.7%; Score 24; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 2.3e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 10 QRGPGRAF 17

Db 4 RRGTGAV 11

RESULT 14

S63490
dissimilatory sulfite reductase alpha chain, soluble - Desulfovibrio desulfuricans (frag

C:Species: Desulfovibrio desulfuricans

C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004

C:Accession: S63490

R:Steuber, J.; Arendsen, A.F.; Hagen, W.R.; Kroneck, P.M.H.

Eur. J. Biochem. 233, 873-879, 1995

A:Title: Molecular properties of the dissimilatory sulfite reductase from Desulfovibrio

A:Reference number: S63489; MUID:96085152; PMID:8521853

A:Accession: S63490

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-20 <STE>

A:Cross-references: UNIPROT:Q9R4H4

Query Match 19.7%; Score 24; DB 2; Length 20;
Best Local Similarity 36.4%; Pred. No. 3.2e+03;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 8 RIORGPGRAFV 18

Db 10 QLESQWPSEV 20

RESULT 15

S31427
biliary glycoprotein - human

C:Species: Homo sapiens (man)

C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 07-Feb-1997

C:Accession: S31427

R:Nedellec, P.; Turbide, C.; Barnett, T.R.; Beauchemin, N.

submitted to the EMBL Data Library, July 1992

A:Description: Characterization of the human biliary glycoprotein regulatory region.

A:Reference number: S31427

A:Accession: S31427

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-21 <NED>

A:Cross-references: EMBL:X67277

C:Keywords: glycoprotein

Query Match 19.7%; Score 24; DB 2; Length 21;
Best Local Similarity 80.0%; Pred. No. 3.3e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 13 PGRAF 17

Db 14 PGRGF 18

Search completed: June 3, 2005, 03:21:13

Job time : 44 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 3, 2005, 03:03:22 ; Search time 171 Seconds
(without alignments)
71.871 Million cell updates/sec

Title: SEQ1

Perfect score: 122

Sequence: 1 nntksirirgpggrafvtigkig 24

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 16988

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 250 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	65	53.3	23	Q9E8S7 human immun
2	63	51.6	25	Q9AQX9 human immun
3	63	51.6	25	Q9AQY0 human immun
4	59	48.4	25	O10481 human immun
5	53	43.4	25	Q9AQY1 human immun
6	53	43.4	25	Q9AQY2 human immun
7	51	41.8	25	Q9QEX7 human immun
8	45	36.9	25	Q7ZJT3 human immun
9	39	32.0	18	Q9PXF1 human immun
10	38	31.1	23	Q9ENM9 human immun
11	33	27.0	22	Q6U2M7 sechium edu
12	29	23.8	20	Q7R974 plasmodium
13	28	23.0	16	Q9RQ46 buchiera ap
14	28	23.0	16	Q9R411 spiropasma
15	27	22.1	16	Q9UCK9 homo sapien
16	27	22.1	16	Q9UCL0 homo sapien
17	27	22.1	17	Q16228 homo sapien
18	27	22.1	19	Q6EML0 meleagris g
19	27	22.1	19	Q6EML1 gallus gall
20	27	22.1	22	Q924C7 mus musculus
21	26.5	21.7	14	Q7M1W9 arabidopsis
22	26	21.3	13	Q7M3F5 oryctolagus
23	26	21.3	14	Q7PE81 anopheles g
24	26	21.3	17	Q9RSN0 bacillus su
25	26	21.3	17	Q78324 human immun
26	26	21.3	18	Q9ZG65 chlamydia t
27	26	21.3	20	Q6JCN3 escherichia
28	26	21.3	21	Q95K54 ovis aries
29	26	21.3	21	Q6RCX2 pseudomonas
30	26	21.3	22	Q7Z992 schizosacch
31	26	21.3	23	Q6U2M9 momordica c

32	26	21.3	24	Q6TQT6	Q6TQT6 saccharomyc
33	26	21.3	24	Q6U2N2	Q6U2N2 citrullus l
34	26	21.3	24	Q9RQ50	Q9RQ50 buchiera ap
35	26	21.3	25	Q69EY6	Q69EY6 lycopersico
36	25	20.5	10	Q7M1V8	Q7M1V8 nicotiana p
37	25	20.5	12	Q84038	Q84038 influenza a
38	25	20.5	13	Q6TUI7	Q6TUI7 ascaris suu
39	25	20.5	14	Q9P2A2	Q9P2A2 homo sapien
40	25	20.5	14	Q85662	Q85662 reovirus ty
41	25	20.5	15	Q86576	Q86576 seborranea
42	25	20.5	16	Q9UCJ7	Q9UCJ7 homo sapien
43	25	20.5	16	Q9TRQ9	Q9TRQ9 sus scrofa
44	25	20.5	17	Q78326	Q78326 human immun
45	25	20.5	19	Q90630	Q90630 cercopithe
46	25	20.5	19	Q90633	Q90633 cercopithe
47	25	20.5	19	Q90R12	Q90R12 human immun
48	25	20.5	20	Q9PWO4	Q9PWO4 gallus gall
49	25	20.5	22	Q6V0X7	Q6V0X7 serratia ma
50	25	20.5	22	Q9AH71	Q9AH71 neisseria m
51	25	20.5	24	1 FCLJ_PACGO	P82421 pachycondyl
52	25	20.5	24	1 FCL2_PACGO	P82422 pachycondyl
53	24.5	20.1	17	Q7M2M8	Q7M2M8 bos taurus
54	24.5	20.1	24	Q89021	Q89021 mus musculu
55	24.5	20.1	25	Q9TWN6	Q9TWN6 theileria e
56	24	19.7	11	Q780C5	Q780C5 neurospora
57	24	19.7	15	Q8TCS7	Q8TCS7 homo sapien
58	24	19.7	15	Q69173	Q69173 yersinia pe
59	24	19.7	16	Q48387	Q48387 klebsiella
60	24	19.7	17	Q78345	Q78345 human immun
61	24	19.7	17	Q78378	Q78378 human immun
62	24	19.7	19	Q84859	Q84859 unidentified
63	24	19.7	19	Q8U0H2	Q8U0H2 gallus gall
64	24	19.7	19	Q8UVE0	Q8UVE0 gallus gall
65	24	19.7	20	Q7RM33	Q7RM33 plasmodium
66	24	19.7	20	Q9R4H4	Q9R4H4 desulfovibr
67	24	19.7	21	CSPS_STRTR	P81622 streptococc
68	24	19.7	24	Q9R4A4	Q9R4A4 oerskovia x
69	24	19.7	25	1 BLP4_BOMOR	P29005 bombina ori
70	24	19.7	25	1 OCE1_LEPOE	P83951 leptodactyl
71	23.5	19.3	16	Q8JH96	Q8JH96 anthus spin
72	23.5	19.3	16	Q8JH97	Q8JH97 anthus prat
73	23.5	19.3	21	Q9TRK1	Q9TRK1 canis fami
74	23.5	19.3	22	Q85524	Q85524 chlamydia t
75	23	18.9	10	1 COXO_RAT	P80432 rattus norv
76	23	18.9	15	1 UC19_MAIZE	P80625 zea mays (m
77	23	18.9	15	Q6TXW1	Q6TXW1 babesia ovi
78	23	18.9	15	Q7WUF8	Q7WUF8 pseudomonas
79	23	18.9	16	Q6XA08	Q6XA08 equus cabal
80	23	18.9	17	1 FATS_ANASP	P82748 anabaena sp
81	23	18.9	17	Q91352	Q91352 gallus gall
82	23	18.9	17	Q78374	Q78374 human immun
83	23	18.9	17	Q78381	Q78381 human immun
84	23	18.9	19	1 TRP3_LEUMA	P81735 leucophaea
85	23	18.9	20	Q51558	Q51558 pseudomonas
86	23	18.9	20	Q7M195	Q7M195 thermus aqu
87	23	18.9	21	Q46419	Q46419 chlamydia t
88	23	18.9	22	Q7S0M0	Q7S0M0 neurospora
89	23	18.9	22	Q9R4Y8	Q9R4Y8 staphylococ
90	23	18.9	22	Q7ZPQ0	Q7ZPQ0 human immun
91	23	18.9	22	Q7ZPQ2	Q7ZPQ2 human immun
92	23	18.9	22	Q9QEX6	Q9QEX6 human immun
93	23	18.9	23	Q61341	Q61341 panulirus i
94	23	18.9	23	Q94781	Q94781 trypanosoma
95	23	18.9	23	Q9R4U4	Q9R4U4 yersinia ps
96	23	18.9	24	Q9TRK0	Q9TRK0 bos taurus
97	23	18.9	24	Q71J04	Q71J04 lactobacill
98	23	18.9	24	Q7M132	Q7M132 treponema h
99	23	18.9	25	1 FLB1_TREHY	P80158 treponema h
100	23	18.4	25	1 SODC_PAROL	P83129 paralichthy
101	22.5	18.4	14	1 TKN1_SCHGR	P82470 schistocerc
102	22.5	18.4	17	Q78328	Q78328 human immun
103	22.5	18.4	20	Q9U8M6	Q9U8M6 liodrosophi
104	22	18.0	10	Q76V19	Q76V19 lactococcus

105	22	18.0	10	2	Q9QVK8	Q9qvks mus sp. mep	178	21	17.2	17	1	MDH ACIDE	P80540 acidovorax
106	22	18.0	14	2	Q16045	Q16045 homo sapien	179	21	17.2	17	2	Q6EML4	Q6eml4 meleagris g
107	22	18.0	14	2	O10226	O10226 human immun	180	21	17.2	17	2	Q6EML5	Q6eml5 gallus gall
108	22	18.0	14	2	O10227	O10227 human immun	181	21	17.2	17	2	Q78323	Q78323 human immun
109	22	18.0	14	2	O10228	O10228 human immun	182	21	17.2	17	2	Q78327	Q78327 human immun
110	22	18.0	14	2	O10232	O10232 human immun	183	21	17.2	17	2	Q78380	Q78380 human immun
111	22	18.0	14	2	O10233	O10233 human immun	184	21	17.2	17	2	Q14042	Q14042 homo sapien
112	22	18.0	15	2	Q66174	Q66174 borrelia ga	185	21	17.2	18	2	Q75M23	Q75m23 mus musculu
113	22	18.0	16	2	Q9TQY6	Q9tqy6 oryctolagus	186	21	17.2	18	2	Q8VDM2	Q8vdm2 mus musculu
114	22	18.0	16	2	Q55090	Q55090 shigella so	187	21	17.2	18	2	Q9VDM2	Q9vdm2 mus musculu
115	22	18.0	17	2	Q9SMC7	Q9smc7 lycopersico	188	21	17.2	18	2	Q90790	Q90790 gallus gall
116	22	18.0	17	2	Q9R575	Q9r575 synecocyst	189	21	17.2	19	1	CUCN CUCNA	P84158 cucurbita m
117	22	18.0	18	1	PCG5_PACGO	P82419 pachycondyl	190	21	17.2	19	2	Q8K5B7	Q8k5b7 rattus norv
118	22	18.0	19	1	PCG5_PACGO	P82420 pachycondyl	191	21	17.2	20	1	MCRG METTE	Q80514 human immun
119	22	18.0	19	2	Q55069	Q55069 synecocyst	192	21	17.2	20	2	Q7R9Q5	P22950 methanosarc
120	22	18.0	19	2	Q62996	Q62996 rattus norv	193	21	17.2	20	2	P82689	P759q5 plasmodium
121	22	18.0	19	2	Q9CVG4	Q9cvg4 mus musculu	194	21	17.2	20	2	Q8S8H8	Q8s8h8 podospora a
122	22	18.0	19	2	Q905E4	Q905e4 human immun	195	21	17.2	20	2	Q9SM31	Q9sm31 triticum ae
123	22	18.0	19	2	Q905G4	Q905g4 human immun	196	21	17.2	20	2	Q8KU19	Q8kui9 neisseria m
124	22	18.0	20	1	CD4_SHEEP	P05442 ovis aries	197	21	17.2	20	2	Q8KU19	Q8kui9 rhodococcus
125	22	18.0	20	1	DFTS_RAT	P07448 rattus norv	198	21	17.2	20	2	Q9PXE4	Q9pjql rhodococcus
126	22	18.0	20	1	EFTU MYCSY	P81407 mycoplasma	199	21	17.2	20	2	Q9PXE4	Q9pxe4 foot-and-mo
127	22	18.0	20	2	Q7S7I7	Q7s7i7 neurospora	200	21	17.2	20	2	Q9PXE4	Q9pxe4 foot-and-mo
128	22	18.0	20	2	Q9TRB9	Q9trb9 bos taurus	201	21	17.2	21	2	Q9PXE4	Q9pxe4 foot-and-mo
129	22	18.0	20	2	Q9TRB9	Q9trb9 bos taurus	202	21	17.2	21	2	Q9PXE4	Q9pxe4 foot-and-mo
130	22	18.0	20	2	Q6LCU3	Q6lcu3 morganella	203	21	17.2	21	2	Q9PXE4	Q9pxe4 foot-and-mo
131	22	18.0	20	2	Q9EQX8	Q9eqx8 mus musculu	204	21	17.2	21	2	Q9PXE4	Q9pxe4 foot-and-mo
132	22	18.0	21	2	Q9H428	Q9h428 homo sapien	205	21	17.2	21	2	Q9PXE4	Q9pxe4 foot-and-mo
133	22	18.0	21	2	Q64LJ1	Q64lj1 gorilla gor	206	21	17.2	21	2	Q9PXE4	Q9pxe4 foot-and-mo
134	22	18.0	21	2	Q9R890	Q9r890 chlamydia t	207	21	17.2	22	2	Q9PXE4	Q9pxe4 foot-and-mo
135	22	18.0	21	2	Q88229	Q88229 mus musculu	208	21	17.2	22	2	Q9PXE4	Q9pxe4 foot-and-mo
136	22	18.0	21	2	Q9R204	Q9r204 mus musculu	209	21	17.2	22	2	Q9PXE4	Q9pxe4 foot-and-mo
137	22	18.0	22	2	P82939	P82939 hordeum vul	210	21	17.2	22	2	Q9PXE4	Q9pxe4 foot-and-mo
138	22	18.0	22	2	Q52435	Q52435 burkholderi	211	21	17.2	22	2	Q9PXE4	Q9pxe4 foot-and-mo
139	22	18.0	22	2	Q616B1	Q616b1 escherichia	212	21	17.2	22	2	Q9PXE4	Q9pxe4 foot-and-mo
140	22	18.0	22	2	Q8X365	Q8x365 escherichia	213	21	17.2	22	2	Q9PXE4	Q9pxe4 foot-and-mo
141	22	18.0	23	1	YPMH_BACSU	Q34890 bacillus su	214	21	17.2	22	2	Q9PXE4	Q9pxe4 foot-and-mo
142	22	18.0	23	2	Q9ZG66	Q9zg66 chlamydia t	215	21	17.2	22	2	Q9PXE4	Q9pxe4 foot-and-mo
143	22	18.0	24	1	TFIS_BOMMO	Q92204 bombyx mori	216	21	17.2	22	2	Q9PXE4	Q9pxe4 foot-and-mo
144	22	18.0	24	2	Q7RJY9	Q7rjy9 plasmodium	217	21	17.2	22	2	Q9PXE4	Q9pxe4 foot-and-mo
145	22	18.0	24	2	Q7ZBU6	Q7zbu6 human immun	218	21	17.2	22	2	Q9PXE4	Q9pxe4 foot-and-mo
146	22	18.0	25	1	RA1C_RANCL	P82875 rana clamit	219	21	17.2	22	2	Q9PXE4	Q9pxe4 foot-and-mo
147	22	18.0	25	1	RAN1_RANCA	P82741 rana catesb	220	21	17.2	23	2	Q9PXE4	Q9pxe4 foot-and-mo
148	22	18.0	25	1	VGT_BPG4	P03652 bacterioph	221	21	17.2	23	2	Q9PXE4	Q9pxe4 foot-and-mo
149	22	18.0	25	2	Q7PGE4	Q7pgf4 anopheles g	222	21	17.2	23	2	Q9PXE4	Q9pxe4 foot-and-mo
150	22	18.0	25	2	Q8MGS5	Q8mg5 sus scrofa	223	21	17.2	23	2	Q9PXE4	Q9pxe4 foot-and-mo
151	22	18.0	25	2	Q7M219	Q7m219 triticum tu	224	21	17.2	23	2	Q9PXE4	Q9pxe4 foot-and-mo
152	22	18.0	25	2	Q60839	Q60839 mus musculu	225	21	17.2	23	2	Q9PXE4	Q9pxe4 foot-and-mo
153	22	18.0	25	2	Q71UFS	Q71uf5 rattus norv	226	21	17.2	23	2	Q9PXE4	Q9pxe4 foot-and-mo
154	22	18.0	25	2	O11890	O11890 gb virus c/	227	21	17.2	23	2	Q9PXE4	Q9pxe4 foot-and-mo
155	22	18.0	25	2	O11891	O11891 gb virus c/	228	21	17.2	23	2	Q9PXE4	Q9pxe4 foot-and-mo
156	22	18.0	25	2	O11893	O11893 gb virus c/	229	21	17.2	23	2	Q9PXE4	Q9pxe4 foot-and-mo
157	22	18.0	25	2	Q66MS0	Q66ms0 human immun	230	21	17.2	24	2	Q9PXE4	Q9pxe4 foot-and-mo
158	21.5	17.6	22	2	Q9TQY9	Q9tqy9 sus scrofa	231	21	17.2	24	2	Q9PXE4	Q9pxe4 foot-and-mo
159	21.5	17.6	22	2	Q02830	Q02830 oryctolagus	232	21	17.2	24	2	Q9PXE4	Q9pxe4 foot-and-mo
160	21.5	17.6	23	2	Q98YR7	Q98yr7 human immun	233	21	17.2	24	2	Q9PXE4	Q9pxe4 foot-and-mo
161	21.5	17.6	24	2	Q9UC38	Q9uc38 homo sapien	234	21	17.2	24	2	Q9PXE4	Q9pxe4 foot-and-mo
162	21	17.2	9	2	Q92012	Q92012 mus musculu	235	21	17.2	25	1	BT12_BOOMI	Q3045 archaeoglob
163	21	17.2	10	1	COXO_THUOB	P80982 thunnus obe	236	21	17.2	25	1	SP1G_PSEUS	Q3045 archaeoglob
164	21	17.2	13	2	Q7M1G8	Q7m1g8 avena sativ	237	21	17.2	25	2	Q9167	Q49167 methanobact
165	21	17.2	13	2	Q27373	Q27373 trypanosoma	238	21	17.2	25	2	Q9167	Q49167 methanobact
166	21	17.2	14	2	Q27373	Q27373 trypanosoma	239	21	17.2	25	2	Q9167	Q49167 methanobact
167	21	17.2	15	2	Q7SH11	Q7sh11 neurospora	240	21	17.2	25	2	Q9167	Q49167 methanobact
168	21	17.2	15	2	Q81ZK4	Q81zk4 homo sapien	241	21	17.2	25	2	Q9167	Q49167 methanobact
169	21	17.2	15	2	Q26825	Q26825 trypanosoma	242	21	17.2	25	2	Q9167	Q49167 methanobact
170	21	17.2	15	2	P82430	P82430 nicotiana t	243	21	17.2	25	2	Q9167	Q49167 methanobact
171	21	17.2	15	2	Q93LE6	Q93le6 chloroflexu	244	21	17.2	25	2	Q9167	Q49167 methanobact
172	21	17.2	16	2	Q16350	Q16350 homo sapien	245	21	17.2	25	2	Q9167	Q49167 methanobact
173	21	17.2	16	2	Q6JDN2	Q6jdn2 canis famil	246	21	17.2	25	2	Q9167	Q49167 methanobact
174	21	17.2	16	2	Q9G0E9	Q9g0e9 bacterioph	247	21	17.2	25	2	Q9167	Q49167 methanobact
175	21	17.2	16	2	Q9G0E9	Q9g0e9 bacterioph	248	21	17.2	25	2	Q9167	Q49167 methanobact
176	21	17.2	16	2	Q47605	Q47605 escherichia	249	20.5	16.8	15	2	Q9EUP4	Q9eup4 thermus the
177	21	17.2	16	2	Q71Z16	Q71z16 gallus gall	250	20.5	16.8	17	2	Q9EUP4	Q9eup4 thermus the

ALIGNMENTS

RESULT 1

Q9E8S7 PRELIMINARY; PRT; 23 AA.
 AC Q9E8S7;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Envelope glycoprotein (Fragment).
 GN Name=env;
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20411423; PubMed=10954550;
 RX DOI=10.1128/JVI.74.18.8494-8501.2000;
 RA Nelson J.A.E., Baribaud F., Edwards T., Swanstrom R.;
 RT "Patterns of changes in human immunodeficiency virus type 1 V3
 sequence populations late in infection.";
 RL J. Virol. 74:8494-8501(2000).
 DR EMBL; AF155888; AACG9930.1; -.
 DR GO; GO:0019031; C:viral envelope; IEA.
 DR InterPro; IPR011056; Pept_S24_S26_C.
 KW Envelope protein.
 FT NON_TER 1
 FT NON_TER 23
 SQ SEQUENCE 23 AA; 2596 MW; 6C038F27BC0CA1E0 CRC64;

Query Match 53.3%; Score 65; DB 2; Length 23;
 Best Local Similarity 60.9%; Pred. No. 0.0019;
 Matches 14; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

Qy 1 NNTKRSIRIQGPGRAFYATGKI 23
 ||||:|||||
 Db 2 NNTRRSMRI--GPGKAFVATGDI 22

RESULT 2

Q8AQX9 PRELIMINARY; PRT; 25 AA.
 AC Q8AQX9;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Envelope glycoprotein (Fragment).
 GN Name=env;
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22860939; PubMed=14502005;
 RA Freil S.A., Fiscus S.A., Pilcher C.D., Menezes P., Giner J.,
 RA Patrick E., Lennox J.L., Hicks C.B., Bron J.J. Jr., Shugars D.C.;
 RT "Envelope diversity, coreceptor usage and syncytium-inducing phenotype
 of HIV-1 variants in saliva and blood during primary infection.";
 RL AIDS 17:2025-2033(2003).
 DR EMBL; AF536914; AAN63929.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0019031; C:viral envelope; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR000777; GP120.
 KW Envelope protein.
 FT NON_TER 1
 FT NON_TER 25
 SQ SEQUENCE 25 AA; 2749 MW; 9B6E9DACB8D56C0C CRC64;

Query Match 51.6%; Score 63; DB 2; Length 25;
 Best Local Similarity 62.5%; Pred. No. 0.0045;
 Matches 15; Conservative 1; Mismatches 6; Indels 2; Gaps 1;

Qy 1 NNTKRSIRIQGPGRAFYATGKI 24
 ||||:|||||
 Db 2 NNTRRSINI--GPGRAFYATDIIG 23

RESULT 3

Q8AQY0 PRELIMINARY; PRT; 25 AA.
 AC Q8AQY0;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Envelope glycoprotein (Fragment).
 GN Name=env;
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22860939; PubMed=14502005;
 RA Freil S.A., Fiscus S.A., Pilcher C.D., Menezes P., Giner J.,
 RA Patrick E., Lennox J.L., Hicks C.B., Bron J.J. Jr., Shugars D.C.;
 RT "Envelope diversity, coreceptor usage and syncytium-inducing phenotype
 of HIV-1 variants in saliva and blood during primary infection.";
 RL AIDS 17:2025-2033(2003).
 DR EMBL; AF536913; AAN63928.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0019031; C:viral envelope; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR000777; GP120.
 KW Envelope protein.
 FT NON_TER 1
 FT NON_TER 25
 SQ SEQUENCE 25 AA; 2749 MW; 9B6E9DACB8D56C0C CRC64;

Query Match 51.6%; Score 63; DB 2; Length 25;
 Best Local Similarity 62.5%; Pred. No. 0.0045;
 Matches 15; Conservative 1; Mismatches 6; Indels 2; Gaps 1;

Qy 1 NNTKRSIRIQGPGRAFYATGKI 24
 ||||:|||||
 Db 2 NNTRRSINI--GPGRAFYATDIIG 23

RESULT 4

O10481 PRELIMINARY; PRT; 25 AA.
 AC O10481;
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Envelope glycoprotein (Fragment).
 GN Name=env;
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97255649; PubMed=9100996;
 RA Rencher S.D., Lockey T.D., Slobod K.S., Hurwitz J.L.;
 RT "Drift from the GPGRAF HIV-1 envelope V3 crown sequence in a North
 American inner city.";
 RL AIDS Res. Hum. Retroviruses 13:527-528(1997).
 DR EMBL; U81241; AAB53843.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0019031; C:viral envelope; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.

DR InterPro; IPR000777; GP120.
DR InterPro; IPR011056; Pept_S24_S26_C.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1 1
FT NON_TER 25 25
SQ SEQUENCE 25 AA; 2801 MW; 25B1B150CD7C14B6 CRC64;

Query Match 48.4%; Score 59; DB 2; Length 25;
Best Local Similarity 66.7%; Pred. No. 0.021;
Matches 14; Conservative 0; Mismatches 5; Indels 2; Gaps 1;

Qy 1 NNTKRSIRIQGPGRAFVTIG 21
Db 6 NNKRKGIHI--GPGAFYTKG 24

RESULT 5
Q8AQY1 PRELIMINARY; PRT; 25 AA.
AC Q8AQY1
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP MEDLINE=22860939; PubMed=14502005;
RA Freil S.A., Fiscus S.A., Pilcher C.D., Menezes P., Giner J., Shugars D.C.;
RA Patrick E., Lennox J.L., Hicks C.B., Eron J.J. Jr., Shugars D.C.;
RT "Envelope diversity, coreceptor usage and syncytium-inducing phenotype of HIV-1 variants in saliva and blood during primary infection.";
RL AIDS 17:2025-2033(2003).
DR EMBL; AF536912; AANG3927.1; -.
DR GO; GO:0019031; C:viral envelope; IEA.
DR InterPro; IPR000777; GP120.
KW Envelope protein.
FT NON_TER 1 1
FT NON_TER 25 25
SQ SEQUENCE 25 AA; 2601 MW; 71B5A774CE256C09 CRC64;

Query Match 43.4%; Score 53; DB 2; Length 25;
Best Local Similarity 58.3%; Pred. No. 0.22;
Matches 14; Conservative 0; Mismatches 8; Indels 2; Gaps 1;

Qy 1 NNTKRSIRIQGPGRAFVTIG 24
Db 2 NNTKGIHI--GPGAFYGTDIIG 23

RESULT 6
Q8AQY2 PRELIMINARY; PRT; 25 AA.
AC Q8AQY2
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP MEDLINE=22860939; PubMed=14502005;
RA Freil S.A., Fiscus S.A., Pilcher C.D., Menezes P., Giner J., Shugars D.C.;
RA Patrick E., Lennox J.L., Hicks C.B., Eron J.J. Jr., Shugars D.C.;
RT "Envelope diversity, coreceptor usage and syncytium-inducing phenotype of HIV-1 variants in saliva and blood during primary infection.";
RL AIDS 17:2025-2033(2003).
DR EMBL; AF536912; AANG3927.1; -.
DR GO; GO:0019031; C:viral envelope; IEA.
DR InterPro; IPR000777; GP120.
KW Envelope protein.
FT NON_TER 1 1
FT NON_TER 25 25
SQ SEQUENCE 25 AA; 2601 MW; 71B5A774CE256C09 CRC64;

Query Match 43.4%; Score 53; DB 2; Length 25;
Best Local Similarity 58.3%; Pred. No. 0.22;
Matches 14; Conservative 0; Mismatches 8; Indels 2; Gaps 1;

Qy 1 NNTKRSIRIQGPGRAFVTIG 24
Db 2 NNTKGIHI--GPGAFYGTDIIG 23

RESULT 7
Q9QEX7 PRELIMINARY; PRT; 25 AA.
AC Q9QEX7
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP MEDLINE=21103026; PubMed=11170057;
RX DOI=10.1002/1096-9071(200103)63:3<197::AID-JMV1000>3.3.CO;2-G;
RA Lin H.J., Siwak E.B., Lauder I.J., Hollinger F.B.;
RT "Long-term culture of human immunodeficiency virus type 1 resulting in loss of glycosylation sites.";
RL J. Med. Virol. 63:197-202(2001).
DR EMBL; AF178663; AAF04369.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:vital capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
DR InterPro; IPR011056; Pept_S24_S26_C.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1 1
FT NON_TER 25 25
SQ SEQUENCE 25 AA; 2818 MW; 9C6EBA908EB5ED47 CRC64;

Query Match 41.8%; Score 51; DB 2; Length 25;
Best Local Similarity 57.1%; Pred. No. 0.47;
Matches 12; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

Qy 1 NNTKRSIRIQGPGRAFVTIG 21
Db 7 NNTRSIPL--GQGRAWFTTG 25

RESULT 8
Q7ZJT3 PRELIMINARY; PRT; 25 AA.
AC Q7ZJT3
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]

RL AIDS 17:2025-2033(2003).
DR EMBL; AF536911; AANG3926.1; -.
DR GO; GO:0019031; C:viral envelope; IEA.
DR InterPro; IPR000777; GP120.
KW Envelope protein.
FT NON_TER 1 1
FT NON_TER 25 25
SQ SEQUENCE 25 AA; 2601 MW; 71B5A774CE256C09 CRC64;

Query Match 43.4%; Score 53; DB 2; Length 25;
Best Local Similarity 58.3%; Pred. No. 0.22;
Matches 14; Conservative 0; Mismatches 8; Indels 2; Gaps 1;

Qy 1 NNTKRSIRIQGPGRAFVTIG 24
Db 2 NNTKGIHI--GPGAFYGTDIIG 23

RESULT 7
Q9QEX7 PRELIMINARY; PRT; 25 AA.
AC Q9QEX7
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP MEDLINE=21103026; PubMed=11170057;
RX DOI=10.1002/1096-9071(200103)63:3<197::AID-JMV1000>3.3.CO;2-G;
RA Lin H.J., Siwak E.B., Lauder I.J., Hollinger F.B.;
RT "Long-term culture of human immunodeficiency virus type 1 resulting in loss of glycosylation sites.";
RL J. Med. Virol. 63:197-202(2001).
DR EMBL; AF178663; AAF04369.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:vital capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
DR InterPro; IPR011056; Pept_S24_S26_C.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1 1
FT NON_TER 25 25
SQ SEQUENCE 25 AA; 2818 MW; 9C6EBA908EB5ED47 CRC64;

Query Match 41.8%; Score 51; DB 2; Length 25;
Best Local Similarity 57.1%; Pred. No. 0.47;
Matches 12; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

Qy 1 NNTKRSIRIQGPGRAFVTIG 21
Db 7 NNTRSIPL--GQGRAWFTTG 25

RESULT 8
Q7ZJT3 PRELIMINARY; PRT; 25 AA.
AC Q7ZJT3
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]

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RP SEQUENCE FROM N.A.
RX MEDLINE=22439926; PubMed=12552446;
RA Iversen A.K.N., Christiansen C.B., Attermann J., Eugen-Olsen J.,
RA Schulman S., Berntorp E., Ingerslev J., Fugger L., Scheibel E.,
RA Tengborn L., Gerstoft J., Dickmeiss E., Sveigaard A., Skinhoj P.;
RT "Limited protective effect of the CCR5Delta32/CCR5Delta32 genotype on
RT human immunodeficiency virus infection incidence in a cohort of
RL patients with hemophilia and selection for genotypic X4 virus.";
RL J. Infect. Dis. 187:215-225(2003).
DR EMBL; AY150666; AAO61698.1; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0019028; C: viral capsid; IEA.
DR GO; GO:0019031; C: viral envelope; IEA.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 25
SQ SEQUENCE 25 AA; 2790 MW; CB4779D487B698D2 CRC64;

Query Match 36.9%; Score 45; DB 2; Length 25;
Best Local Similarity 50.0%; Pred. No. 4.7;
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 8 RIQRGPGRAFTVIGKI 23
Db 1 RLSMGPGRVVYTGPI 16

RESULT 9
Q9PXF1
ID Q9PXF1 PRELIMINARY; PRT; 18 AA.
AC Q9PXF1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE GP120 protein (Fragment).
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN SEQUENCE FROM N.A.
RP MEDLINE=95386957; PubMed=7658059;
RA Lawko A., Johansson B., Dash R., Falck L., Dietrich U., Pipkorn R.,
RA Nilehn B., Blomberg J.;
RT "Continuity and discontinuity in the anti-V3 IgG response of human
RT immunodeficiency virus type 1-infected persons in a cross-sectional
RT and longitudinal study using synthetic peptides.";
RL J. Infect. Dis. 172:682-690(1995).
SQ SEQUENCE 18 AA; 2047 MW; F5884C2C32F15B55 CRC64;

Query Match 32.0%; Score 39; DB 2; Length 18;
Best Local Similarity 64.3%; Pred. No. 34;
Matches 9; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

Qy 1 NNRKSIRIQRPG 14
Db 7 NNRK--RMTMGPG 18.

RESULT 10
Q9ENM9
ID Q9ENM9 PRELIMINARY; PRT; 23 AA.
AC Q9ENM9;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
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RN SEQUENCE FROM N.A.
RX MEDLINE=20411423; PubMed=10954550;
RA DOI=10.1128/JVI.74.18.8494-8501.2000;
RA Nelson J.A.E., Baribaud F., Edwards T., Swanson R.;
RT "Patterns of changes in human immunodeficiency virus type 1 V3
RT sequence populations late in infection.";
RL J. Virol. 74:8494-8501(2000).
DR EMBL; AF092639; AAO04382.1; -.
DR GO; GO:0019031; C: viral envelope; IEA.
KW Envelope protein.
FT NON_TER 1
FT NON_TER 23
SQ SEQUENCE 23 AA; 2460 MW; 6108AEC9C0CA947 CRC64;

Query Match 31.1%; Score 38; DB 2; Length 23;
Best Local Similarity 58.3%; Pred. No. 65;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 12 GPGRAFTVIGKI 23
Db 11 GPGKAFVATGDI 22

RESULT 11
Q6U2M7
ID Q6U2M7 PRELIMINARY; PRT; 22 AA.
AC Q6U2M7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Galactinol synthase (EC 2.4.1.123) (Fragment).
GN Name=GSI;
OS Sechium edule.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eusoids I; Cucurbitales; Cucurbitaceae; Sechium.
OX NCBI_TaxID=184140;
RN SEQUENCE FROM N.A.
RP MEDLINE=22975109; PubMed=14526110; DOI=10.1104/pp.103.027714;
RA Ayre B.G., Blair J.E., Turgeon R.;
RT "Functional and phylogenetic analyses of a conserved regulatory
RT program in the phloem of minor veins.";
RL Plant Physiol. 133:1229-1239(2003).
DR EMBL; AV379782; AAQ74884.1; -.
DR GO; GO:0047216; F: inositol 3-alpha-galactosyltransferase acti. . .; IEA.
DR GO; GO:0016757; F: transferase activity, transferring glycosyl. . .; IEA.
KW Glycosyltransferase; Transferase.
FT NON_TER 22
SQ SEQUENCE 22 AA; 2295 MW; A6673B5BFD06430C CRC64;

Query Match 27.0%; Score 33; DB 2; Length 22;
Best Local Similarity 47.1%; Pred. No. 4.3e+02;
Matches 8; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Qy 3 TRKSIRIQRPGRAFTV 19
Db 6 TETAESTDAPKRAFTV 22

RESULT 12
Q7R974
ID Q7R974 PRELIMINARY; PRT; 20 AA.
AC Q7R974;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein (Fragment).
GN Name=PY06991;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
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RN SEQUENCE FROM N.A.
RC STRAIN=17XNL;
RX PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Anguolli S.V., Suh B.B., Kooij T.W., Perteau M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallow J.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M.,
RA Florens L., Yates F.R. II, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser R.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii."
RL Nature 419:512-519(2002).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL: AABL01002466; EAA19325.1; -.
KW Hypothetical protein.
FT NON_TER 20
SQ SEQUENCE 20 AA; 2461 MW; C583B1AD3B45C3FC CRC64;

Query Match 23.8%; Score 29; DB 2; Length 20;
Best Local Similarity 41.7%; Pred. No. 1.8e+03;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 7 IRIQGGGPGAPV 18
Db |::|::|::|
9 INMKRGTSRLFI 20

RESULT 13
ID Q9RQ46 PRELIMINARY; PRT; 24 AA.
AC Q9RQ46;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE ATP-dependent DNA helicase (Fragment).
GN Name=rep;
OS Buchnera aphidicola.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Buchnera.
OX NCBI_TaxID=9;

[1]
RN SEQUENCE FROM N.A.
RX PubMed=20022990; PubMed=10555290;
RA Clark M.A., Moran N.A., Baumann P.;
RT "Sequence evolution in bacterial endosymbionts having extreme base
RT compositions."
RL Mol. Biol. Evol. 16:1586-1598(1999).
DR EMBL: AF130814; AAF1308.1; -.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0004003; F:ATP-dependent DNA helicase activity; IEA.
DR GO: GO:0003677; F:DNA binding; IEA.
DR GO: GO:0004386; F:helicase activity; IEA.
DR GO: GO:0006281; P:DNA repair; IEA.
DR InterPro: IPR000212; UvrD-helicase.
DR Pfam: PF00580; UvrD-helicase; 1.
FT NON_TER 24
SQ SEQUENCE 24 AA; 2515 MW; EA88246B840C4B75 CRC64;

Query Match 23.8%; Score 29; DB 2; Length 24;
Best Local Similarity 41.7%; Pred. No. 2.2e+03;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 NTRKSIRIQGP 13
Db |::|::|::|
6 NQKXAVRCISGP 17

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RESULT 14
Q9R4L1 PRELIMINARY; PRT; 16 AA.
ID Q9R4L1;
AC Q9R4L1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE L-lactate dehydrogenase homolog (Fragment).
OS Spiroplasma melliferum.
OC Bacteria; Firmicutes; Mollicutes; Entomoplasmatales;
OC Spiroplasmataceae; Spiroplasma.
OX NCBI_TaxID=21134;
RN [1]
RP SEQUENCE.
RX MEDLINE=953331240; PubMed=7607178;
RA Cordwell S.J., Wilkins M.R., Cerpa-Poljak A., Gooley A.A., Duncan M.,
RA Williams K.L., Humphrey-Smith I.;
RL Electrophoresis 16:438-443(1995).
SQ SEQUENCE 16 AA; 1749 MW; FF2078A15AE1647C CRC64;

Query Match 23.0%; Score 28; DB 2; Length 16;
Best Local Similarity 41.7%; Pred. No. 2.1e+03;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 NNRKSIRIQRG 12
Db |::|::|::|
3 NSTRKVLVGEV 14

RESULT 15
Q9UCK9 PRELIMINARY; PRT; 16 AA.
ID Q9UCK9;
AC Q9UCK9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Serum amyloid A isotype 2 alpha protein (Serum amyloid A protein)
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=93099171; PubMed=1463770; DOI=10.1016/0925-4439(92)90068-X;
RA Baba S., Takahashi T., Kasama T., Shirasawa H.;
RT "Identification of two novel amyloid A protein subsets coexisting in
RT an individual patient of AA-amyloidosis."
RL Biochim. Biophys. Acta 1180:195-200(1992).
DR PIR: A27902; YLHUA.
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0006953; P:acute-phase response; IEA.
DR InterPro: IPR000096; Serum_amyloid_A.
DR Pfam: PF00277; SAA; 1.
DR SEQUENCE 16 AA; 1612 MW; 1CAB4F077C9C8CC1 CRC64;

Query Match 22.1%; Score 27; DB 2; Length 16;
Best Local Similarity 71.4%; Pred. No. 3.1e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 RGPGRAP 17
Db |::|::|::|
1 RGPGGAW 7

Search completed: June 3, 2005, 03:20:35
Job time : 183 secs

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OM protein - protein search, using sw model

Run on: June 3, 2005, 03:12:32 ; Search time 40 Seconds
(without alignments)
44.789 Million cell updates/sec

Title: SEQ1
Perfect score: 122
Sequence: 1 nntksiridrgpgrafvtgkig 24

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 218077

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 250 summaries

Database : Issued Patents AA.*
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3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	122	100.0	24	2	US-08-146-028-160
4	122	100.0	24	3	US-08-723-425A-160
5	122	100.0	24	3	US-08-480-332-2
6	122	100.0	24	3	US-09-112-206-160
7	122	100.0	24	4	US-08-790-497A-14
8	122	100.0	24	4	US-08-790-497A-160
9	122	100.0	24	4	US-08-576-824A-160
10	122	100.0	24	4	US-08-680-497-160
11	122	100.0	24	5	PCT-US92-06688-12
12	122	100.0	24	5	PCT-US92-10378-3
13	122	100.0	25	3	US-08-465-324-13
14	122	100.0	25	3	US-08-485-324-31
15	122	100.0	25	3	US-08-447-506-13
16	122	100.0	25	3	US-08-447-506-31
17	122	100.0	25	3	US-08-235-437-13
18	122	100.0	25	3	US-08-235-437-31
19	122	100.0	25	3	US-08-447-515-13
20	122	100.0	25	3	US-08-447-515-31
21	116	95.1	24	1	US-08-257-528B-99
22	116	95.1	24	1	US-08-460-602A-99
23	116	95.1	24	1	US-08-463-966A-99
24	116	95.1	24	1	US-08-465-217A-99
25	116	95.1	24	2	US-08-464-329A-99
26	116	95.1	24	2	US-08-462-507A-99
27	116	95.1	24	2	US-08-467-881A-99

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29	112	91.8	25	2	US-07-950-571A-1	Sequence 1, Appli
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33	106	86.9	22	3	US-09-070-291-5	Sequence 5, Appli
34	101	82.8	21	2	US-08-452-503A-4	Sequence 4, Appli
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45	101	82.8	21	4	US-09-635-754-25	Sequence 25, Appli
46	101	82.8	21	4	US-08-680-525-25	Sequence 25, Appli
47	101	82.8	21	4	US-09-636-223-25	Sequence 25, Appli
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59	97	79.5	20	3	US-08-973-551-24	Sequence 24, Appli
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61	97	79.5	23	5	PCT-US94-02539-27	Sequence 27, Appli
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65	96	78.7	20	1	US-08-465-217A-51	Sequence 51, Appli
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81	86	70.5	21	1	US-08-465-217A-16	Sequence 16, Appli
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87	85	69.7	17	1	US-08-463-966A-35	Sequence 35, Appli
88	85	69.7	17	1	US-08-465-217A-35	Sequence 35, Appli
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103	77	63.1	15	1	US-08-218-025A-17	Sequence 17, Appl	176	73	59.8	25	3	US-09-112-206-9	Sequence 9, Appl
104	77	63.1	15	1	US-08-709-047-7	Sequence 7, Appl	177	73	59.8	25	3	US-09-112-206-155	Sequence 155, App
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107	77	63.1	15	1	US-08-095-332-1	Sequence 1, Appl	180	72	59.0	14	2	US-08-455-625-9	Sequence 9, Appl
108	77	63.1	15	1	US-08-707-801A-7	Sequence 7, Appl	181	72	59.0	14	2	US-08-455-685-9	Sequence 9, Appl
109	77	63.1	15	1	US-08-709-006-7	Sequence 7, Appl	182	72	59.0	14	3	US-08-060-988A-9	Sequence 9, Appl
110	77	63.1	15	1	US-08-711-175-7	Sequence 7, Appl	183	72	59.0	14	5	PCT-US94-05142-9	Sequence 9, Appl
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117	77	63.1	15	2	US-08-455-625-7	Sequence 7, Appl	190	72	59.0	15	3	US-08-455-685-21	Sequence 21, Appl
118	77	63.1	15	2	US-08-395-204-2	Sequence 2, Appl	191	72	59.0	15	3	US-08-455-685-21	Sequence 21, Appl
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122	77	63.1	15	2	US-08-986-234-28	Sequence 28, Appl	195	72	59.0	15	5	PCT-US94-05142-20	Sequence 20, Appl
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127	77	63.1	15	3	US-08-060-988A-7	Sequence 7, Appl	200	71	58.2	15	2	US-08-455-625-15	Sequence 15, Appl
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131	77	63.1	15	4	US-09-827-688-9	Sequence 9, Appl	204	71	58.2	15	3	US-08-455-685-11	Sequence 11, Appl
132	77	63.1	15	5	PCT-US92-10378-1	Sequence 1, Appl	205	71	58.2	15	3	US-08-455-685-15	Sequence 15, Appl
133	77	63.1	15	5	PCT-US94-05142-7	Sequence 7, Appl	206	71	58.2	15	3	US-08-455-685-16	Sequence 16, Appl
134	76	62.3	15	1	US-08-218-025A-16	Sequence 16, Appl	207	71	58.2	15	3	US-08-455-685-18	Sequence 18, Appl
135	76	62.3	15	1	US-08-704-170-72	Sequence 72, Appl	208	71	58.2	15	3	US-08-455-685-22	Sequence 22, Appl
136	76	62.3	15	5	PCT-US94-02631-72	Sequence 72, Appl	209	71	58.2	15	3	US-08-060-988A-11	Sequence 11, Appl
137	76	62.3	23	3	US-08-513-968-74	Sequence 74, Appl	210	71	58.2	15	3	US-08-060-988A-13	Sequence 13, Appl
138	76	62.3	23	3	US-08-513-968-75	Sequence 75, Appl	211	71	58.2	15	3	US-08-060-988A-15	Sequence 15, Appl
139	76	62.3	23	4	US-09-790-497A-154	Sequence 154, App	212	71	58.2	15	3	US-08-060-988A-16	Sequence 16, Appl
140	76	62.3	23	4	US-08-576-824A-154	Sequence 154, App	213	71	58.2	15	3	US-08-060-988A-18	Sequence 18, Appl
141	76	62.3	25	2	US-08-146-028-7	Sequence 7, Appl	214	71	58.2	15	3	US-08-060-988A-22	Sequence 22, Appl
142	76	62.3	25	2	US-08-146-028-154	Sequence 154, App	215	71	58.2	15	5	PCT-US94-05142-11	Sequence 11, Appl
143	76	62.3	25	3	US-08-723-425A-7	Sequence 7, Appl	216	71	58.2	15	5	PCT-US94-05142-13	Sequence 13, Appl
144	76	62.3	25	3	US-09-112-206-7	Sequence 154, App	217	71	58.2	15	5	PCT-US94-05142-15	Sequence 15, Appl
145	76	62.3	25	3	US-08-112-206-6	Sequence 7, Appl	218	71	58.2	15	5	PCT-US94-05142-16	Sequence 16, Appl
146	76	62.3	25	3	US-08-112-206-154	Sequence 154, App	219	71	58.2	15	5	PCT-US94-05142-18	Sequence 18, Appl
147	76	62.3	25	4	US-09-680-497-7	Sequence 7, Appl	220	71	58.2	15	5	PCT-US94-05142-22	Sequence 22, Appl
148	76	62.3	25	4	US-08-680-497-154	Sequence 154, App	221	71	58.2	24	1	US-08-218-025A-134	Sequence 134, App
149	75	61.5	15	1	US-08-704-170-70	Sequence 70, Appl	222	71	58.2	24	1	US-08-306-116A-16	Sequence 16, Appl
150	75	61.5	15	5	PCT-US94-02631-70	Sequence 70, Appl	223	71	58.2	25	1	US-08-125-012-14	Sequence 14, Appl
151	74	60.7	15	2	US-08-455-625-12	Sequence 12, Appl	224	71	58.2	25	2	US-08-783-818-14	Sequence 14, Appl
152	74	60.7	15	3	US-08-455-685-12	Sequence 12, Appl	225	71	58.2	25	2	US-08-453-349-14	Sequence 14, Appl
153	74	60.7	15	3	US-08-060-988A-12	Sequence 12, Appl	226	71	58.2	25	2	US-08-979-385B-12	Sequence 12, Appl
154	74	60.7	15	5	PCT-US94-05142-12	Sequence 12, Appl	227	71	58.2	25	4	US-08-860-576-14	Sequence 14, Appl
155	74	60.7	19	1	US-08-279-906A-19	Sequence 19, Appl	228	71	58.2	23	3	US-08-513-968-73	Sequence 73, Appl
156	74	60.7	23	3	US-08-513-968-71	Sequence 71, Appl	229	70	57.4	23	3	US-08-455-625-14	Sequence 14, Appl
157	74	60.7	23	3	US-08-513-968-71	Sequence 71, Appl	230	69	56.6	15	2	US-08-455-685-14	Sequence 14, Appl
158	73	59.8	14	1	US-08-090-148-4	Sequence 4, Appl	231	69	56.6	15	3	US-08-060-988A-14	Sequence 14, Appl
159	73	59.8	15	2	US-08-455-625-17	Sequence 17, Appl	232	69	56.6	15	5	PCT-US94-05142-14	Sequence 14, Appl
160	73	59.8	15	2	US-08-455-625-23	Sequence 23, Appl	233	69	56.6	15	5	PCT-US94-05142-14	Sequence 14, Appl
161	73	59.8	15	2	US-08-455-685-17	Sequence 17, Appl	234	68	55.7	13	1	US-08-090-148-5	Sequence 5, Appl
162	73	59.8	15	3	US-08-455-685-23	Sequence 23, Appl	235	68	55.7	13	1	US-08-279-906A-17	Sequence 17, Appl
163	73	59.8	15	3	US-08-060-988A-17	Sequence 17, Appl	236	68	55.7	14	2	US-08-455-625-10	Sequence 10, Appl
164	73	59.8	15	3	US-08-060-988A-23	Sequence 23, Appl	237	68	55.7	14	3	US-08-455-685-10	Sequence 10, Appl
165	73	59.8	15	5	PCT-US94-05142-17	Sequence 17, Appl	238	68	55.7	14	3	US-08-060-988A-10	Sequence 10, Appl
166	73	59.8	22	2	US-08-345-321-17	Sequence 17, Appl	239	68	55.7	14	5	PCT-US94-05142-10	Sequence 10, Appl
167	73	59.8	22	3	US-08-513-968-72	Sequence 72, Appl	240	68	55.7	22	2	US-08-345-321-22	Sequence 22, Appl
168	73	59.8	23	3	US-09-790-497A-155	Sequence 155, App	241	68	55.7	22	4	US-09-790-497A-9	Sequence 9, Appl
169	73	59.8	23	4	US-08-576-824A-155	Sequence 155, App	242	66.5	54.5	22	4	US-09-576-824A-7	Sequence 7, Appl
170	73	59.8	23	4	US-08-345-321-12	Sequence 12, Appl	243	66.5	54.5	24	4	US-09-576-824A-9	Sequence 9, Appl
171	73	59.8	24	2	US-08-146-028-9	Sequence 9, Appl	244	66	54.1	13	1	US-08-488-252-25	Sequence 25, Appl
172	73	59.8	25	2	US-08-146-028-9	Sequence 9, Appl	245	66	54.1	13	2	US-08-657-392-19	Sequence 19, Appl
173	73	59.8	25	2	US-08-146-028-155	Sequence 155, App	246	66	54.1	13			

247 66 54.1 13 2 US-08-657-392-20 Sequence 20, Appl
248 66 54.1 13 2 US-08-657-392-21 Sequence 21, Appl
249 66 54.1 13 2 US-08-657-392-23 Sequence 23, Appl
250 66 54.1 13 5 PCT-US94-02539-19 Sequence 19, Appl

ALIGNMENTS

RESULT 1
US-08-097-751-1
; Sequence 1, Application US/08097751
; Patent No. 5527666
; GENERAL INFORMATION:
; APPLICANT: Derossi, Anita
; APPLICANT: Pasti, Marcella
; APPLICANT: Mammano, Fabrizio
; APPLICANT: Panozzo, Maria
; APPLICANT: Dettin, Monica
; APPLICANT: DiBello, Carlo
; APPLICANT: Chiesco-Bianchi, Luigi
; TITLE OF INVENTION: METHOD FOR THE DIAGNOSIS IN VITRO OF
; TITLE OF INVENTION: HIV-1 VIRUS INFECTIONS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hedman, Gibson, Costigan & Hoare
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: DOS
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/097,751
; FILING DATE: 19930723
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Costigan, James V.
; REGISTRATION NUMBER: 25,669
; REFERENCE/DOCKET NUMBER: 515-4026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 302-8989
; TELEFAX: (212) 302-8998
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
; US-08-097-751-1

Query Match 100.0%; Score 122; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNTKRSIRIQGPGRAFTVIGKIG 24
Db 1 NNTKRSIRIQGPGRAFTVIGKIG 24

RESULT 2
US-08-090-148-6
; Sequence 6, Application US/08090148
; Patent No. 5534257
; GENERAL INFORMATION:
; APPLICANT: Mastico, Robert Allan
; APPLICANT: Stockley, Peter George

; APPLICANT: Talbot, Simon John
; TITLE OF INVENTION: Antigen-Presenting Capsid with
; TITLE OF INVENTION: Fusion MS2-Coat Protein
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rosenman & Colin
; STREET: 575 Madison Avenue
; CITY: New York
; STATE: NY
; COUNTRY: U.S.A.
; ZIP: 10022-2585
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5", 1.44Mb
; COMPUTER: IBM PS2-486
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/090,148
; FILING DATE: 08/11/93
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9101550.3
; FILING DATE: 01/24/93
; APPLICATION NUMBER: PCT/GB92/00124
; FILING DATE: 01/22/92
; ATTORNEY/AGENT INFORMATION:
; NAME: Nissenbaum, Israel
; REGISTRATION NUMBER: 27,582
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 940-8636
; TELEFAX: (212) 940-6404
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 AMINO ACIDS
; TYPE: AMINO ACID
; TOPOLOGY: NOT RELEVANT
; MOLECULE TYPE: PEPTIDE
; US-08-090-148-6

Query Match 100.0%; Score 122; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNTKRSIRIQGPGRAFTVIGKIG 24
Db 1 NNTKRSIRIQGPGRAFTVIGKIG 24

RESULT 3
US-08-146-028-160
; Sequence 160, Application US/08146028
; Patent No. 5891640
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES
; TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR
; TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED
; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,
; TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM
; NUMBER OF SEQUENCES: 453
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

US-08-146-028-160
; Sequence 160, Application US/08146028
; Patent No. 5891640
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES
; TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR
; TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED
; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,
; TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM
; NUMBER OF SEQUENCES: 453
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

US-08-090-148-6
; Sequence 6, Application US/08090148
; Patent No. 5534257
; GENERAL INFORMATION:
; APPLICANT: Mastico, Robert Allan
; APPLICANT: Stockley, Peter George

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; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-146-028-160

Query Match 100.0%; Score 122; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNTRKSIRIQRGPRAFVTIGKIG 24
Db 1 NNTRKSIRIQRGPRAFVTIGKIG 24

RESULT 4
US-08-723-425A-160
; Sequence 160, Application US/08723425A
; Patent No. 6165730
; GENERAL INFORMATION:
; APPLICANT: DELEYS, ROBERT
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF
; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT
; TITLE OF INVENTION: EPITOPES AND THEIR USE IN A PROCESS FOR DETERMINATION OF
; TITLE OF INVENTION: ANTIBODIES OR BIOTINYLATED PEPTIDES CORRESPONDING ...
; NUMBER OF SEQUENCES: 453
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHVE, P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/723,425A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 1487-13
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 160:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-723-425A-160

Query Match 100.0%; Score 122; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNTRKSIRIQRGPRAFVTIGKIG 24
Db 1 NNTRKSIRIQRGPRAFVTIGKIG 24

RESULT 5
US-08-480-332-2
; Sequence 2, Application US/08480332
; Patent No. 6180134
; GENERAL INFORMATION:
; APPLICANT: Zalipsky, Samuel; Woodie, Martin; Francis;
; APPLICANT: Barenholz, Yechezkel
; TITLE OF INVENTION: Enhanced Circulation Effector Composition and
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; TITLE OF INVENTION: Method
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,332
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/316,436
; FILING DATE: 29-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/035,443
; FILING DATE: 23-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Mohr, Judy M.
; REGISTRATION NUMBER: 38,563
; REFERENCE/DOCKET NUMBER: 5325-0115.31
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Peptide 2, Fig. 13
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..15
; US-08-480-332-2

Query Match 100.0%; Score 122; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNTRKSIRIQRGPRAFVTIGKIG 24
Db 1 NNTRKSIRIQRGPRAFVTIGKIG 24

RESULT 6
US-09-112-206-160
; Sequence 160, Application US/09112206
; Patent No. 6210903
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES
; TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR
; TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED
; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,
; TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM
; NUMBER OF SEQUENCES: 453
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/112.206
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/146,028
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 160:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-112-206-160

Query Match      100.0%; Score 122; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNTKRSIRIQGPGRAFTVIGKIG 24
   |||||
Db 1 NNTKRSIRIQGPGRAFTVIGKIG 24

RESULT 7
US-09-790-497A-14
; Sequence 14, Application US/09790497A
; Patent No. 6649735
; GENERAL INFORMATION:
; APPLICANT: De Leye, Robert
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES CORRESPONDING
; TITLE OF INVENTION: TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR USE IN
; TITLE OF INVENTION: A PROCESS FOR DETERMINATION OF ANTIBODIES OF
; TITLE OF INVENTION: BIOTINYLATED PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT
; TITLE OF INVENTION: EPITOPES, A PROCESS FOR PREPARING THEM AND COMPOSITIONS
; TITLE OF INVENTION: CONTAINING THEM
; FILE REFERENCE: 2752-16
; CURRENT APPLICATION NUMBER: US/09/790,497A
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 09/576,824
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 08/723,425
; PRIOR FILING DATE: 1996-09-30
; PRIOR APPLICATION NUMBER: 09/146,028
; PRIOR FILING DATE: 1993-11-22
; PRIOR APPLICATION NUMBER: PCT/EP93/00517
; PRIOR FILING DATE: 1993-03-08
; PRIOR APPLICATION NUMBER: EP 92400598.6
; PRIOR FILING DATE: 1992-03-06
; NUMBER OF SEQ ID NOS: 600
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
; US-09-790-497A-14

Query Match      100.0%; Score 122; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNTKRSIRIQGPGRAFTVIGKIG 24
   |||||
Db 1 NNTKRSIRIQGPGRAFTVIGKIG 24

RESULT 8
US-09-790-497A-160
; Sequence 160, Application US/09790497A
; Patent No. 6649735
; GENERAL INFORMATION:
; APPLICANT: De Leye, Robert
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES CORRESPONDING
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; TITLE OF INVENTION: TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR USE IN
; TITLE OF INVENTION: A PROCESS FOR DETERMINATION OF ANTIBODIES OF
; TITLE OF INVENTION: BIOTINYLATED PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT
; TITLE OF INVENTION: EPITOPES, A PROCESS FOR PREPARING THEM AND COMPOSITIONS
; TITLE OF INVENTION: CONTAINING THEM
; FILE REFERENCE: 2752-16
; CURRENT APPLICATION NUMBER: US/09/790,497A
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 09/576,824
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 08/723,425
; PRIOR FILING DATE: 1996-09-30
; PRIOR APPLICATION NUMBER: 09/146,028
; PRIOR FILING DATE: 1993-11-22
; PRIOR APPLICATION NUMBER: PCT/EP93/00517
; PRIOR FILING DATE: 1993-03-08
; PRIOR APPLICATION NUMBER: EP 92400598.6
; PRIOR FILING DATE: 1992-03-06
; NUMBER OF SEQ ID NOS: 600
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 160
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
; US-09-790-497A-160

Query Match      100.0%; Score 122; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNTKRSIRIQGPGRAFTVIGKIG 24
   |||||
Db 1 NNTKRSIRIQGPGRAFTVIGKIG 24

RESULT 9
US-09-576-824A-160
; Sequence 160, Application US/09576824A
; Patent No. 6667387
; GENERAL INFORMATION:
; APPLICANT: De Leye, Robert
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES CORRESPONDING
; TITLE OF INVENTION: TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR USE IN
; TITLE OF INVENTION: A PROCESS FOR DETERMINATION OF ANTIBODIES OF
; TITLE OF INVENTION: BIOTINYLATED PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT
; TITLE OF INVENTION: EPITOPES, A PROCESS FOR PREPARING THEM AND COMPOSITIONS
; TITLE OF INVENTION: CONTAINING THEM
; FILE REFERENCE: 2752-11
; CURRENT APPLICATION NUMBER: US/09/576,824A
; CURRENT FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 08/723,425
; PRIOR FILING DATE: 1996-09-30
; PRIOR APPLICATION NUMBER: 09/146,028
; PRIOR FILING DATE: 1993-11-22
; PRIOR APPLICATION NUMBER: PCT/EP93/00517
; PRIOR FILING DATE: 1993-03-08
; PRIOR APPLICATION NUMBER: EP 92400598/6
; PRIOR FILING DATE: 1992-03-06
; NUMBER OF SEQ ID NOS: 600
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 160
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
; US-09-576-824A-160

Query Match      100.0%; Score 122; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNTKRSIRIQGPGRAFTVIGKIG 24
   |||||
Db 1 NNTKRSIRIQGPGRAFTVIGKIG 24
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; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00231/052W01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24
; TYPE: AMINO ACID
; TOPOLOGY: linear
; PCT-US92-06688-12

Query Match      100.0%   Score 122: DB 5: Length 24;
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Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps

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; Sequence 3, Application PC/TUS9210378
; GENERAL INFORMATION:
; APPLICANT: BOARD OF REGENTS, THE UNIVERSITY OF
; APPLICANT: TEXAS SYSTEM
; APPLICANT: SASTRY, Jagannadha K.
; APPLICANT: ARLINGHAUS, Ralph B.
; APPLICANT: PLATSOUCAS, Chris D.
; APPLICANT: NEHETE, Pramod N.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS
; TITLE OF INVENTION: FOR ELICITING IMMUNE OR ANTI-INFECTION RESPONSES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: US
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
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; APPLICATION NUMBER: PCT/US92/10378
; FILING DATE: 19921202
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/800,932
; FILING DATE: December 2, 1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/945865
; FILING DATE: September 16, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, David L.
; REGISTRATION NUMBER: 32,165
; REFERENCE/DOCKET NUMBER: UTFC305PCT/
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-320-7200
; TELEFAX: 512-474-7577
; TELEX: Not Applicable
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PCT-US92-10378-3

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Query Match 100.0%; Score 122; DB 5; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 13

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; Sequence 13, Application US/08485324
; Patent No. 6043093
; GENERAL INFORMATION:
; APPLICANT: Wohlstadter, Jacob
; TITLE OF INVENTION: SELECTION METHODS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris, & Safford
; ADDRESSEE: c/o Barry Evans
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,324
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/235,437
; FILING DATE: 29-APR-1994
; APPLICATION NUMBER: US 07/852,412
; FILING DATE: 16-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Evans, Barry
; REGISTRATION NUMBER: 22,802
; REFERENCE/DOCKET NUMBER: 370132-2000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-485-324-13

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Db 1 NNTKSIIRIQGPGRAFTVIGKIG 24

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US-08-485-324-31
; Sequence 31, Application US/08485324
; Patent No. 6043093
; GENERAL INFORMATION:
; APPLICANT: Wohlstadter, Jacob
; TITLE OF INVENTION: SELECTION METHODS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Curtis, Morris, & Safford
ADDRESSEE: c/o Barry Evans
STREET: 530 Fifth Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,324
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/235,437
FILING DATE: 29-APR-1994
APPLICATION NUMBER: US 07/852,412
FILING DATE: 16-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Evans, Barry
REGISTRATION NUMBER: 22,802
REFERENCE/DOCKET NUMBER: 370132-2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-485-324-31

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; Patent No. 6066499
; GENERAL INFORMATION:
; APPLICANT: Wohlstadter, Jacob
; TITLE OF INVENTION: SELECTION METHODS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris, & Safford
; ADDRESSEE: c/o Barry Evans
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,506
FILING DATE: 23-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/235,437
FILING DATE: 29-APR-1994

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Fri Jun 3 06:53:20 2005

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; APPLICATION NUMBER: US 07/852,412
; FILING DATE: 16-MAR-1992
; ATTORNEY/AGENT INFORMATION:
;   NAME: Evans, Barry
;   REGISTRATION NUMBER: 22,802
;   REFERENCE/DOCKET NUMBER: 370132-2000
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (212) 840-3333
;   TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 13:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 25 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
; US-08-447-506-13

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GenCore version 5.1.6
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OM protein - protein search, using sw model

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Perfect score: 122

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 250 summaries

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Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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124	48	39.3	18	14	US-10-059-271-25	Sequence 25, Appl	197	40	32.8	17	16	US-10-677-074-12	Sequence 12, Appl
125	48	39.3	18	14	US-10-059-271-27	Sequence 27, Appl	198	40	32.8	17	16	US-10-805-913-6	Sequence 6, Appli
126	48	39.3	18	14	US-09-825-886-30	Sequence 30, Appl	199	40	32.8	17	16	US-09-964-201A-16	Sequence 16, Appl
127	47	38.5	9	17	US-10-494-161-17	Sequence 17, Appl	200	39	32.0	12	10	US-10-431-596-81	Sequence 81, Appl
128	47	38.5	9	17	US-09-956-940-51	Sequence 51, Appl	201	39	32.0	12	15	US-10-681-389-16	Sequence 16, Appl
129	47	38.5	10	15	US-10-360-647A-18	Sequence 18, Appl	202	39	32.0	12	16	US-10-681-388-16	Sequence 16, Appl
130	46	37.7	15	15	US-10-622-003-11	Sequence 11, Appl	203	39	32.0	12	16	US-09-810-310-32	Sequence 32, Appl
131	46	37.7	15	17	US-10-613-018-23	Sequence 23, Appl	204	39	32.0	15	9	US-10-442-909-42	Sequence 42, Appl
132	46	37.7	18	17	US-10-613-018-41	Sequence 41, Appl	205	39	32.0	15	17	US-10-622-003-10	Sequence 10, Appl
133	46	37.7	18	17	US-10-613-018-42	Sequence 42, Appl	206	39	32.0	16	14	US-10-018-986-141	Sequence 141, App
134	46	37.7	23	17	US-10-621-675-163	Sequence 163, App	207	39	32.0	16	14	US-10-655-702-3	Sequence 3, Appli
135	46	37.7	25	17	US-10-621-675-17	Sequence 17, Appl	208	38	31.1	10	9	US-09-810-310-17	Sequence 17, Appl
136	46	37.7	25	17	US-10-373-592-109	Sequence 109, App	209	38	31.1	10	9	US-09-810-310-17	Sequence 17, Appl
137	45.5	37.3	24	15	US-10-079-167-52	Sequence 52, Appl	210	38	31.1	12	9	US-09-873-459A-3	Sequence 3, Appli
138	45	36.9	9	14	US-10-360-836-49	Sequence 49, Appl	211	38	31.1	12	14	US-10-016-986-48	Sequence 48, Appl
139	45	36.9	9	14	US-10-367-580-115	Sequence 115, App	212	38	31.1	12	14	US-10-448-546-3	Sequence 3, Appli
140	45	36.9	9	15	US-10-367-593-115	Sequence 115, App	213	38	31.1	12	14	US-10-654-200-41	Sequence 41, Appl
141	45	36.9	9	15	US-10-367-594-115	Sequence 115, App	214	38	31.1	14	16	US-10-654-200-92	Sequence 92, Appl
142	45	36.9	9	15	US-10-367-654-115	Sequence 115, App	215	38	31.1	14	16	US-10-654-200-90	Sequence 90, Appl
143	45	36.9	9	15	US-10-367-658-115	Sequence 115, App	216	38	31.1	15	16	US-10-059-271-26	Sequence 26, Appl
144	45	36.9	9	15	US-10-367-668-115	Sequence 115, App	217	38	31.1	19	14	US-10-059-271-26	Sequence 26, Appl
145	45	36.9	9	16	US-10-367-674-115	Sequence 115, App	218	38	31.1	21	16	US-10-654-200-91	Sequence 91, Appl
146	45	36.9	9	16	US-10-653-624-52	Sequence 52, Appl	219	37	30.3	13	14	US-10-213-742-6	Sequence 6, Appli
147	45	36.9	9	16	US-10-833-439-52	Sequence 52, Appl	220	37	30.3	17	14	US-10-059-271-20	Sequence 20, Appl
148	45	36.9	9	16	US-10-833-745-52	Sequence 52, Appl	221	37	30.3	22	14	US-10-029-386-34214	Sequence 34214, A
149	45	36.9	9	16	US-10-833-744-52	Sequence 52, Appl	222	36	29.5	9	16	US-10-777-053-305	Sequence 305, App
150	45	36.9	12	15	US-10-431-596-80	Sequence 80, Appl	223	36	29.5	10	9	US-09-810-310-23	Sequence 23, Appl
151	45	36.9	15	15	US-10-338-592-11	Sequence 11, Appl	224	36	29.5	10	9	US-09-810-310-20	Sequence 20, Appl
152	45	36.9	15	17	US-10-622-003-3	Sequence 3, Appli	225	36	29.5	10	9	US-09-087-513-18	Sequence 18, Appl
153	45	36.9	15	17	US-10-622-003-13	Sequence 13, Appl	226	36	29.5	15	9	US-09-810-310-28	Sequence 28, Appl
154	45	36.9	15	17	US-10-628-004-9	Sequence 9, Appli	227	36	29.5	24	14	US-10-080-608A-71	Sequence 71, Appl
155	45	36.9	20	17	US-10-628-004-10	Sequence 10, Appl	228	36	29.5	24	15	US-10-371-067-2	Sequence 2, Appli
156	45	36.9	24	15	US-10-373-592-110	Sequence 110, App	229	35.5	29.1	9	10	US-09-997-848A-17	Sequence 17, Appl
157	45	36.9	12	15	US-10-431-596-78	Sequence 78, Appl	230	35	28.7	10	9	US-09-775-805-6	Sequence 6, Appli
158	44	36.1	13	14	US-10-213-742-1	Sequence 1, Appli	231	35	28.7	10	14	US-10-200-708-627	Sequence 627, App
159	44	36.1					232						

233 Sequence 15, Appl
 234 Sequence 21, Appl
 235 Sequence 247, App
 236 Sequence 6, Appl
 237 Sequence 29, Appl
 238 Sequence 245, App
 239 Sequence 34, Appl
 240 Sequence 5, Appl
 241 Sequence 37, Appl
 242 Sequence 16, Appl
 243 Sequence 15, Appl
 244 Sequence 7, Appl
 245 Sequence 52, Appl
 246 Sequence 4, Appl
 247 Sequence 36, Appl
 248 Sequence 60, Appl
 249 Sequence 18, Appl
 250 Sequence 78, Appl

ALIGNMENTS

RESULT 1
 US-10-621-675-160
 ; Sequence 160, Application US/10621675
 ; Publication No. US20050049398A1
 ; GENERAL INFORMATION:
 ; APPLICANT: De Leys, Robert
 ; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES CORRESPONDING
 ; TITLE OF INVENTION: TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR USE IN
 ; TITLE OF INVENTION: A PROCESS FOR DETERMINATION OF ANTIBODIES OF
 ; TITLE OF INVENTION: BIOTINYLATED PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT
 ; TITLE OF INVENTION: EPITOPES, A PROCESS FOR PREPARING THEM AND COMPOSITIONS
 ; TITLE OF INVENTION: CONTAINING THEM
 ; FILE REFERENCE: 2752-11
 ; CURRENT APPLICATION NUMBER: US/10/621,675
 ; CURRENT FILING DATE: 2003-07-18
 ; PRIOR APPLICATION NUMBER: US/09/576,824A
 ; PRIOR FILING DATE: 08/723,425
 ; PRIOR FILING DATE: 1996-09-30
 ; PRIOR APPLICATION NUMBER: 09/146,028
 ; PRIOR FILING DATE: 1993-11-22
 ; PRIOR APPLICATION NUMBER: PCT/EP93/00517
 ; PRIOR FILING DATE: 1993-03-08
 ; PRIOR APPLICATION NUMBER: EP 92400598.6
 ; PRIOR FILING DATE: 1992-03-06
 ; NUMBER OF SEQ ID NOS: 600
 ; SOFTWARE: PatentIn ver. 2.1
 ; SEQ ID NO 160
 ; LENGTH: 24
 ; TYPE: PRT
 ; ORGANISM: Human immunodeficiency virus
 US-10-621-675-160

Query Match 100.0%; Score 122; DB 17; Length 24;
 Best Local Similarity 100.0%; Pred. No. 8.8e-12;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNTKRSIRIQGPGRAFVTIGKIG 24
 Db 1 NNTKRSIRIQGPGRAFVTIGKIG 24

RESULT 2
 US-10-876-343A-13
 ; Sequence 13, Application US/10876343A
 ; Publication No. US20050106560A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wohlstadter, Jacob N
 ; TITLE OF INVENTION: Selection Methods
 ; FILE REFERENCE: 100405-02121
 ; CURRENT APPLICATION NUMBER: US/10/876,343A

; CURRENT FILING DATE: 2004-06-23
 ; PRIOR APPLICATION NUMBER: US 09/573,830
 ; PRIOR FILING DATE: 2000-05-18
 ; PRIOR APPLICATION NUMBER: US 6,087,177
 ; PRIOR FILING DATE: 1994-04-29
 ; NUMBER OF SEQ ID NOS: 31
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 13
 ; LENGTH: 25
 ; TYPE: PRT
 ; ORGANISM: Artificial
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic HIV gp120, variable region 3, aa 271-295
 US-10-876-343A-13

Query Match 100.0%; Score 122; DB 17; Length 25;
 Best Local Similarity 100.0%; Pred. No. 9.2e-12;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNTKRSIRIQGPGRAFVTIGKIG 24
 Db 1 NNTKRSIRIQGPGRAFVTIGKIG 24

RESULT 3
 US-10-876-343A-31
 ; Sequence 31, Application US/10876343A
 ; Publication No. US20050106560A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wohlstadter, Jacob N
 ; TITLE OF INVENTION: Selection Methods
 ; FILE REFERENCE: 100405-02121
 ; CURRENT APPLICATION NUMBER: US/10/876,343A
 ; CURRENT FILING DATE: 2004-06-23
 ; PRIOR APPLICATION NUMBER: US 09/573,830
 ; PRIOR FILING DATE: 2000-05-18
 ; PRIOR APPLICATION NUMBER: US 6,087,177
 ; PRIOR FILING DATE: 1994-04-29
 ; NUMBER OF SEQ ID NOS: 31
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 31
 ; LENGTH: 25
 ; TYPE: PRT
 ; ORGANISM: Artificial
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic HIV gp120, variable region 3, aa 271-295
 US-10-876-343A-31

Query Match 100.0%; Score 122; DB 17; Length 25;
 Best Local Similarity 100.0%; Pred. No. 9.2e-12;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNTKRSIRIQGPGRAFVTIGKIG 24
 Db 1 NNTKRSIRIQGPGRAFVTIGKIG 24

RESULT 4
 US-10-178-488-25
 ; Sequence 25, Application US/10178488
 ; Publication No. US20030165535A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rovinski, Benjamin
 ; APPLICANT: Cao, Shi-Xian
 ; APPLICANT: Yao, Fei-Long
 ; APPLICANT: Persson, Roy
 ; APPLICANT: Klein, Michel H.
 ; TITLE OF INVENTION: RETROVIRUS-LIKE PARTICLES MADE NON-INFECTIONOUS BY A
 ; TITLE OF INVENTION: PLURALITY OF MUTATIONS
 ; FILE REFERENCE: 1038-1238 MIS
 ; CURRENT APPLICATION NUMBER: US/10/178,488
 ; CURRENT FILING DATE: 2002-10-25
 ; PRIOR APPLICATION NUMBER: 09/258,128


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RESULT 8
US-10-311-111-1
; Sequence 1, Application US/10311111
; Publication No. US20030121065A1
; GENERAL INFORMATION:
; APPLICANT: SHIBA, KIYOTAKA
; TITLE OF INVENTION: MULTIFUNCTIONAL BASE SEQUENCE AND ARTIFICIAL GENE CONTAINING THE
; FILE REFERENCE: 4439-4004
; CURRENT APPLICATION NUMBER: US/10/311,111
; CURRENT FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: JP 2000-180997
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 20
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Designed peptide
US-10-311-111-1
Query Match 77.9%; Score 95; DB 14; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.1e-07;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 RKSIRIQRGPGRAFTVIGKI 23
Db 1 RKSIRIQRGPGRTFTVIGKI 20

RESULT 9
US-10-398-932-1
; Sequence 1, Application US/10398932
; Publication No. US20040171803A1
; GENERAL INFORMATION:
; APPLICANT: SHIBA, KIYOTAKA
; APPLICANT: OHNO, TSUNEYA
; TITLE OF INVENTION: ARTIFICIAL PROTEINS WITH ENRICHED IMMUNOGEN
; TITLE OF INVENTION: OF EPITOPE
; FILE REFERENCE: 024918-0103
; CURRENT APPLICATION NUMBER: US/10/398,932
; CURRENT FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: PCT/JP01/08893
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: JP 2000/314288
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetically Designed
US-10-398-932-1
Query Match 77.9%; Score 95; DB 16; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.1e-07;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 RKSIRIQRGPGRAFTVIGKI 23
Db 1 RKSIRIQRGPGRTFTVIGKI 20

RESULT 10
US-10-062-710-45
; Sequence 45, Application US/10062710
; Publication No. US20030049253A1
; GENERAL INFORMATION:
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; APPLICANT: Li, Frank Q.
; APPLICANT: Chu, Yong-Liang
; APPLICANT: Qiu, Jian-Tai
; TITLE OF INVENTION: Polymeric Conjugates for Delivery of
; TITLE OF INVENTION: MHC-Recognized Epitopes
; TITLE OF INVENTION: Via Peptide Vaccines
; FILE REFERENCE: 3781-001-27
; CURRENT APPLICATION NUMBER: US/10/062,710
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: US 60/310,498
; PRIOR FILING DATE: 2001-08-08
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HIV Helper-T Cell Epitopes
US-10-062-710-45
Query Match 67.2%; Score 82; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 IQRGPGRAFTVIGKI 24
Db 2 IQRGPGRAFTVIGKI 17

RESULT 11
US-09-810-310-15
; Sequence 15, Application US/09810310
; Patent No. US2002004948A1
; GENERAL INFORMATION:
; APPLICANT: Khleif, Samir N.
; APPLICANT: Berzofsky, Jay A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CO-STIMULATION OF
; TITLE OF INVENTION: IMMUNOLOGICAL RESPONSES TO PEPTIDE ANTIGENS
; FILE REFERENCE: 15280-415100US
; CURRENT APPLICATION NUMBER: US/09/810,310
; CURRENT FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/189,396
; PRIOR FILING DATE: 2000-03-15
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV PEPTIDE
US-09-810-310-15
Query Match 63.1%; Score 77; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 RIQRGPGRAFTVIGK 22
Db 1 RIQRGPGRAFTVIGK 15

RESULT 12
US-09-810-310-24
; Sequence 24, Application US/09810310
; Patent No. US2002004948A1
; GENERAL INFORMATION:
; APPLICANT: Khleif, Samir N.
; APPLICANT: Berzofsky, Jay A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CO-STIMULATION OF
; TITLE OF INVENTION: IMMUNOLOGICAL RESPONSES TO PEPTIDE ANTIGENS
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; FILE REFERENCE: 15280-415100US
; CURRENT APPLICATION NUMBER: US/09/810,310
; CURRENT FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/189,396
; PRIOR FILING DATE: 2000-03-15
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV PEPTIDE
; OTHER INFORMATION: ANTIGEN
US-09-810-310-24

Query Match      63.1%; Score 77; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 RIQGGGCGRAFTVIGK 22
Db      1 RIQGGGCGRAFTVIGK 15

RESULT 13
US-09-989-621-8
; Sequence 8, Application US/09989621
; Patent No. US20020151683A1
; GENERAL INFORMATION:
; APPLICANT: Mogam Biotechnology Research Institute
; APPLICANT: Kim, Tae-Youn
; APPLICANT: Lee, Ki-Young
; APPLICANT: Chang, Jin-Soo
; APPLICANT: Cho, Sung-Yoo
; APPLICANT: Hwang, Yu-Kyeong
; APPLICANT: Choi, Myeong
; APPLICANT: Cheong, Hong-Seok
; TITLE OF INVENTION: Liposomes Comprising Peptide Antigens
; TITLE OF INVENTION: Derived from X Protein of Hepatitis B virus
; FILE REFERENCE: 0136/0E154
; CURRENT APPLICATION NUMBER: US/09/989,621
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 09/051,006
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 15
; TYPE: PRT
; ORGANISM: HIV
US-09-989-621-8

Query Match      63.1%; Score 77; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 RIQGGGCGRAFTVIGK 22
Db      1 RIQGGGCGRAFTVIGK 15

RESULT 14
US-09-827-688-9
; Sequence 9, Application US/09827688
; Publication No. US20030165476A1
; GENERAL INFORMATION:
; APPLICANT: ORSON, FRANK
; APPLICANT: KINSEY, BERMA
; APPLICANT: BHOGAL, BALR
; TITLE OF INVENTION: MACROAGGREGATED PROTEIN CONJUGATES AS ORAL GENETIC IMMUNIZATION
; TITLE OF INVENTION: AGENTS
; FILE REFERENCE: P01949US1/10004014
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; CURRENT APPLICATION NUMBER: US/09/827,688
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/195,680
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 15
; TYPE: PRT
; ORGANISM: HIV p18
US-09-827-688-9

Query Match      63.1%; Score 77; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 RIQGGGCGRAFTVIGK 22
Db      1 RIQGGGCGRAFTVIGK 15

RESULT 15
US-09-077-439A-3
; Sequence 3, Application US/09077439A
; Publication No. US20030202989A1
; GENERAL INFORMATION:
; APPLICANT: Collier, R. John
; APPLICANT: Blank, Steven R.
; APPLICANT: Milne, Jill C.
; APPLICANT: Benson, Ericka L.
; APPLICANT: Ballard, Jimmy D.
; APPLICANT: Starnbach, Michael N.
; TITLE OF INVENTION: Use of Toxin Peptides and/or Affinity
; TITLE OF INVENTION: Handles for Delivering Compounds into Cells
; FILE REFERENCE: 00246/187002
; CURRENT APPLICATION NUMBER: US/09/077,439A
; CURRENT FILING DATE: 1999-04-08
; PRIOR APPLICATION NUMBER: PCT/US96/20463
; PRIOR FILING DATE: 1996-12-13
; PRIOR APPLICATION NUMBER: US 60/019,275
; PRIOR FILING DATE: 1996-06-07
; PRIOR APPLICATION NUMBER: US 60/008,518
; PRIOR FILING DATE: 1995-12-13
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-077-439A-3

Query Match      63.1%; Score 77; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 RIQGGGCGRAFTVIGK 22
Db      1 RIQGGGCGRAFTVIGK 15

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(plural,
syncytia)

Multi-nucleate cells formed by the fusion of neighboring cells. Syncytia may form due to the expression of a viral fusion protein during viral replication.

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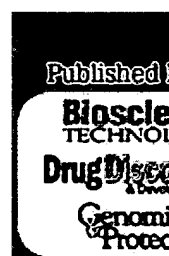
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- Cellular Imagi

Bioscience E



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Result No.	Score	Query Match	Length	DB ID	Description
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2	122	100.0	24	2	AAR07018 Residues
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4	122	100.0	24	2	AAR29233 Heterocon
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6	122	100.0	24	2	AAR32406 Sequence
7	122	100.0	24	2	AAR38165 V3 loop p
8	122	100.0	24	2	AAY22581 HIV LDL b
9	122	100.0	24	3	AAB15873 Human che
10	122	100.0	24	4	AAB68602 HIV gp120
11	122	100.0	25	1	AAP90281 Peptide 1
12	122	100.0	25	2	AAR08276 HIV pepti
13	122	100.0	25	2	AAR31276 HIV princ
14	122	100.0	25	2	AAR30031 HIV princ
15	122	100.0	25	2	AAR26712 HIV-PND-p
16	122	100.0	25	2	AAR33222 HIV gp120
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19	120	98.4	25	2	AAR04427 Human imm
20	118	96.7	24	2	AAY22583 HIV LDL b
21	116	95.1	23	2	AAR04502 Cpd. elic
22	116	95.1	24	2	AAR33190 Sequence
23	116	95.1	24	2	AAR67414 HIV-1 pep
24	116	95.1	24	2	AAW98904 HIV-1 vac
25	116	95.1	24	2	AAY39769 HIV1 chim

seq1.rag

Fri Jun 3 06:53:20 2005

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102	81	66.4	21	3	ABJ5012	Peptide p	175	73	59.8	19	2	AAR60663	HTLV-LAV-III
103	80	65.6	21	3	AAR33236	HIV-IIIB	176	73	59.8	19	2	AAR60655	HTLV-IIIB
104	80	65.6	17	2	AAR76848	Fusion im	177	73	59.8	19	2	AAR60655	HTLV-IIIB
105	80	65.6	18	2	AAR38526	Cyclic HI	178	73	59.8	19	2	AAW16501	SP-10 reg
106	80	65.6	18	2	AAR38526	Cyclic HI	179	73	59.8	19	2	AAW16501	SP-10 reg
107	79	64.8	16	8	ADR18865	HIV LDL b	180	73	59.8	19	2	AAW73236	SP-10 III
108	79	64.8	22	2	AAV22589	Antigenic	181	73	59.8	19	6	ABU07506	HIV glyco
109	78	63.9	15	1	AAV22589	Antigenic	182	73	59.8	19	6	ABU07506	HIV glyco
110	78	63.9	19	2	AAW4928	Fusion im	183	73	59.8	20	2	AAW76895	Fusion im
111	78	63.9	20	2	AAW4928	Fusion im	184	73	59.8	20	2	AAW73258	SP-10 lik
112	78	63.9	21	2	AAW79180	Fusion im	185	73	59.8	20	2	AAW73258	SP-10 lik
113	78	63.9	21	1	AAW76901	Fusion im	186	73	59.8	20	2	AAW73258	SP-10 lik
114	77	63.1	15	1	AAW82095	Env-K1 pe	187	73	59.8	22	2	AAW73258	SP-10 lik
115	77	63.1	15	1	AAW82095	Env-K1 pe	188	73	59.8	22	2	AAW73258	SP-10 lik
116	77	63.1	15	1	AAW82095	Env-K1 pe	189	73	59.8	22	2	AAW73258	SP-10 lik
117	77	63.1	15	2	AAW82095	Env-K1 pe	190	72	59.0	14	2	AAW76896	Fusion im
118	77	63.1	15	2	AAW82095	Env-K1 pe	191	72	59.0	14	2	AAW76896	Fusion im
119	77	63.1	15	2	AAW82095	Env-K1 pe	192	72	59.0	15	2	AAW76896	Fusion im
120	77	63.1	15	2	AAW82095	Env-K1 pe	193	72	59.0	15	2	AAW76896	Fusion im
121	77	63.1	15	2	AAW82095	Env-K1 pe	194	72	59.0	15	2	AAW76896	Fusion im
122	77	63.1	15	2	AAW82095	Env-K1 pe	195	72	59.0	15	2	AAW76896	Fusion im
123	77	63.1	15	2	AAW82095	Env-K1 pe	196	72	59.0	15	2	AAW76896	Fusion im
124	77	63.1	15	2	AAW82095	Env-K1 pe	197	72	59.0	15	3	AAW85592	HIV pepi
125	77	63.1	15	2	AAW82095	Env-K1 pe	198	72	59.0	15	3	AAW85592	HIV pepi
126	77	63.1	15	2	AAW82095	Env-K1 pe	199	72	59.0	15	3	AAW85592	HIV pepi
127	77	63.1	15	2	AAW82095	Env-K1 pe	200	72	59.0	15	3	AAW85592	HIV pepi
128	77	63.1	15	2	AAW82095	Env-K1 pe	201	72	59.0	15	3	AAW85592	HIV pepi
129	77	63.1	15	2	AAW82095	Env-K1 pe	202	71	58.2	15	2	AAW66425	HIV-1 V3
130	77	63.1	15	2	AAW82095	Env-K1 pe	203	71	58.2	15	2	AAW66425	HIV-1 V3
131	77	63.1	15	2	AAW82095	Env-K1 pe	204	71	58.2	15	2	AAW66425	HIV-1 V3
132	77	63.1	15	2	AAW82095	Env-K1 pe	205	71	58.2	15	2	AAW66425	HIV-1 V3
133	77	63.1	15	2	AAW82095	Env-K1 pe	206	71	58.2	15	2	AAW66425	HIV-1 V3
134	77	63.1	15	2	AAW82095	Env-K1 pe	207	71	58.2	15	2	AAW66425	HIV-1 V3
135	77	63.1	15	2	AAW82095	Env-K1 pe	208	71	58.2	15	2	AAW66425	HIV-1 V3
136	77	63.1	15	2	AAW82095	Env-K1 pe	209	71	58.2	15	2	AAW66425	HIV-1 V3
137	77	63.1	15	2	AAW82095	Env-K1 pe	210	71	58.2	15	2	AAW66425	HIV-1 V3
138	77	63.1	15	2	AAW82095	Env-K1 pe	211	71	58.2	15	2	AAW66425	HIV-1 V3
139	77	63.1	15	2	AAW82095	Env-K1 pe	212	71	58.2	15	2	AAW66425	HIV-1 V3
140	77	63.1	15	2	AAW82095	Env-K1 pe	213	71	58.2	15	2	AAW66425	HIV-1 V3
141	77	63.1	15	2	AAW82095	Env-K1 pe	214	71	58.2	15	2	AAW66425	HIV-1 V3
142	77	63.1	15	2	AAW82095	Env-K1 pe	215	71	58.2	15	2	AAW66425	HIV-1 V3
143	77	63.1	15	2	AAW82095	Env-K1 pe	216	71	58.2	15	2	AAW66425	HIV-1 V3
144	77	63.1	15	2	AAW82095	Env-K1 pe	217	71	58.2	15	2	AAW66425	HIV-1 V3
145	77	63.1	15	2	AAW82095	Env-K1 pe	218	71	58.2	15	2	AAW66425	HIV-1 V3
146	77	63.1	15	2	AAW82095	Env-K1 pe	219	71	58.2	15	2	AAW66425	HIV-1 V3
147	77	63.1	15	2	AAW82095	Env-K1 pe	220	71	58.2	15	2	AAW66425	HIV-1 V3
148	77	63.1	15	2	AAW82095	Env-K1 pe	221	71	58.2	15	2	AAW66425	HIV-1 V3
149	77	63.1	15	2	AAW82095	Env-K1 pe	222	71	58.2	15	2	AAW66425	HIV-1 V3
150	77	63.1	15	2	AAW82095	Env-K1 pe	223	71	58.2	15	2	AAW66425	HIV-1 V3
151	77	63.1	15	2	AAW82095	Env-K1 pe	224	71	58.2	15	2	AAW66425	HIV-1 V3
152	77	63.1	15	2	AAW82095	Env-K1 pe	225	71	58.2	15	2	AAW66425	HIV-1 V3
153	77	63.1	15	2	AAW82095	Env-K1 pe	226	71	58.2	15	2	AAW66425	HIV-1 V3
154	77	63.1	15	2	AAW82095	Env-K1 pe	227	71	58.2	15	2	AAW66425	HIV-1 V3
155	77	63.1	15	2	AAW82095	Env-K1 pe	228	71	58.2	15	2	AAW66425	HIV-1 V3
156	77	63.1	15	2	AAW82095	Env-K1 pe	229	71	58.2	15	2	AAW66425	HIV-1 V3
157	77	63.1	15	2	AAW82095	Env-K1 pe	230	71	58.2	15	2	AAW66425	HIV-1 V3
158	77	63.1	15	2	AAW82095	Env-K1 pe	231	71	58.2	15	2	AAW66425	HIV-1 V3
159	77	63.1	15	2	AAW82095	Env-K1 pe	232	71	58.2	15	2	AAW66425	HIV-1 V3
160	77	63.1	15	2	AAW82095	Env-K1 pe	233	71	58.2	15	2	AAW66425	HIV-1 V3
161	77	63.1	15	2	AAW82095	Env-K1 pe	234	71	58.2	15	2	AAW66425	HIV-1 V3
162	77	63.1	15	2	AAW82095	Env-K1 pe	235	71	58.2	15	2	AAW66425	HIV-1 V3
163	77	63.1	15	2	AAW82095	Env-K1 pe	236	71	58.2	15	2	AAW66425	HIV-1 V3
164	77	63.1	15	2	AAW82095	Env-K1 pe	237	71	58.2	15	2	AAW66425	HIV-1 V3
165	77	63.1	15	2	AAW82095	Env-K1 pe	238	71	58.2	15	2	AAW66425	HIV-1 V3
166	77	63.1	15	2	AAW82095	Env-K1 pe	239	71	58.2	15	2	AAW66425	HIV-1 V3
167	77	63.1	15	2	AAW82095	Env-K1 pe	240	71	58.2	15	2	AAW66425	HIV-1 V3
168	77	63.1	15	2	AAW82095	Env-K1 pe	241	71	58.2	15	2	AAW66425	HIV-1 V3
169	77	63.1	15	2	AAW82095	Env-K1 pe	242	71	58.2	15	2	AAW66425	HIV-1 V3
170	77	63.1	15	2	AAW82095	Env-K1 pe	243	71	58.2	15	2	AAW66425	HIV-1 V3
171	77	63.1	15	2	AAW82095	Env-K1 pe	244	71	58.2	15	2	AAW66425	HIV-1 V3

245 66 54.1 15 2 AAR40198 Sequence
 246 66 54.1 15 2 AAR60675 HTLV SP-1
 247 66 54.1 15 2 AAR58606 Alkaline
 248 66 54.1 15 2 AAR85382 HTLV-III
 249 66 54.1 15 2 AAR85382
 250 66 54.1 15 2 AAW16525 SP-10 C r
 AAW73255 SP-10 C r

ALIGNMENTS

RESULT 1
 AAR06211
 ID AAR06211 standard; peptide; 24 AA.

XX AC AAR06211;
 DT 10-DEC-1990 (first entry)
 XX DE Immunosuppressant protease inhibitor.
 XX KW Organ transplant; autoimmune disease; allergy; aplastic anaemia;
 XX KW systemic erythematodes.
 XX OS Synthetic.
 XX PN JP02157229-A.
 XX PD 18-JUN-1990.
 XX PF 07-DEC-1988; 88JP-00310635.
 XX PR 07-DEC-1988; 88JP-00310635.
 XX PA (NITL) NITTO DENKO CORP.
 XX DR WPI; 1990-233739/31.
 XX PT Protease inhibiting peptide immuno-suppressant - used to suppress
 PT rejection reaction in organs transplantation.
 PS Claim 1; Page 181; 6pp; Japanese.

XX CC Protease inhibitor may be used to suppress organ transplant rejection
 CC without serious side effects. It may also be used in prevention and
 CC therapy of allergy, aplastic anaemia and systemic erythematodes. See
 CC also AAR06212

XX SQ Sequence 24 AA;
 Query Match 100.0%; Score 122; DB 2; Length 24;
 Best Local Similarity 100.0%; Pred. No. 2.6e-10;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNTKRSIRIQGPGRAFTVIGKIG 24
 Db 1 NNTKRSIRIQGPGRAFTVIGKIG 24

RESULT 2
 AAR07018
 ID AAR07018 standard; peptide; 24 AA.

XX AC AAR07018;
 DT 24-OCT-2003 (revised)
 XX DT 18-JAN-1991 (first entry)
 XX DE Residues 301-324 of HIV gp 120 protein used in isolation of sulphated
 XX polysaccharide by affinity chromatography.
 XX KW HIV; AIDS; ARC; gp120; RP135.
 XX PT

OS Human immunodeficiency virus 1.
 XX CA2007258-A.
 XX PD 11-JUL-1990.
 XX PF 05-JAN-1990; 90CA-02007258.
 XX PR 11-JAN-1989; 89US-00295856.
 XX PR 05-JUL-1989; 89US-00375795.
 XX PA (RICH) MERRELL DOW PHARM INC.
 XX PI Cardin AD, Jackson RL;
 XX DR WPI; 1990-290631/39.

XX PT Prepn. of anti-HIV sulphated polysaccharide - by affinity chromatography
 XX using a resin-bound peptide corresp. to a HIV gp. 120 fragment.
 XX PS Disclosure; Page ?; 34pp; English.

XX CC Anti-HIV sulphated polysaccharide (SPS) can prevent syncytium formation
 CC in HIV infected C4 cells. SPS may be isolated by affinity chromatography
 CC with the given resin bound peptide fragment RP135. (Updated on 24-OCT-
 CC 2003 to standardise OS field)

XX SQ Sequence 24 AA;

Query Match 100.0%; Score 122; DB 2; Length 24;
 Best Local Similarity 100.0%; Pred. No. 2.6e-10;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNTKRSIRIQGPGRAFTVIGKIG 24
 Db 1 NNTKRSIRIQGPGRAFTVIGKIG 24

RESULT 3
 AAR26565
 ID AAR26565 standard; peptide; 24 AA.

XX AC AAR26565;
 XX DT 24-OCT-2003 (revised)
 XX DT 25-MAR-2003 (revised)
 XX DT 28-JAN-1993 (first entry)

XX DE Sequence of peptide DB1 determined from the V3 principal neutralising
 DE domain (PND) region of HIV-1 strain HTLV-III B.

XX KW Diagnostic; assay; detection; AIDS; human immunodeficiency virus.

XX OS Human immunodeficiency virus 1; strain HTLV-III B.

XX PN W09213882-A1.

XX PD 20-AUG-1992.

XX PF 29-JAN-1992; 92WO-EF000187.

XX PR 30-JAN-1991; 91IT-MI000220.

XX PA (SUPE-) INST SUPERIORE DI SANITA.
 XX (CNDR) CONSIGLIO NAZ DELLE RICERCHE.

XX PI De Rossi A, Pasti M, Mammano F, Panozzo M, Dettin M, Di Bello C;
 XX Chieco-Bianchi L;

XX DR WPI; 1992-299983/36.

XX PT Synthetic peptide(s) which enhance infectivity of HIV-1 in cellular
 PT cultures - are used for determining HIV-1 virus in blood and other

RESOLUC
AAR32406

CC may be either unconjugated or conjugated to an immunogenic carrier, eg.
CC keyhole limpet hemocyanin (KLH) or ovalbumin, using succinyl

ID AAR32406 standard; peptide; 24 AA.
 AC AAR32406;
 XX
 DT 25-MAR-2003 (revised)
 DT 04-JUL-1993 (first entry)
 XX
 DE Sequence of peptide B1 which comprises AAs 308-331 from the V3 region of
 DE HIV-1 isolate IIIB.
 XX
 KW HIV-1; vaccine; dendritic core; ss.
 XX
 OS Synthetic.
 XX
 PN WO9303766-A1.
 XX
 PD 04-MAR-1993.
 XX
 PF 11-AUG-1992; 92WO-US006688.
 XX
 PR 13-AUG-1991; 91US-00744281.
 XX
 PA (BEPK) REPLIGEN CORP.
 PA (UYRQ) UNIV ROCKEFELLER.
 XX
 PI Tam JP, Profy AT;
 XX
 DR WPI; 1993-093730/11.
 XX
 PR New multiple antigen peptide(s) as HIV vaccines - include a dendritic
 PT core covalently bonded to peptide including the sequence IGPR.
 XX
 PR Example; Fig 1; 35pp; English.
 PS
 CC Nine peptides from the V3 regions of HIV-1 isolates IIIB, RF and MN were
 CC incorporated into tetraivalent multiple antigen peptide systems (MAPS)
 CC (see AAR32406-14). Parallel groups of three peptides with chain lengths
 CC spanning from 11-24 residues were synthesised in MAPS format for each
 CC isolate. ELIS assays demonstrated that antisera titers in mice were
 CC closely related to the length of the IIIB peptide used for the
 CC immunisation - the longer the stronger the response. There was no
 CC substantial antibody prodn. in mice against the other two series of
 CC peptides, RF (B4-B6), and MN (B7-B9), except for a low reactivity in the
 CC gp. immunised with B8 (MN isolate). Specificity tests of the B cell
 CC response demonstrated that the T cell epitope (AAR32415) also serves as a
 CC B cell epitope. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 24 AA;
 Query Match 100.0%; Score 122; DB 2; Length 24;
 Best Local Similarity 100.0%; Pred. No. 2.6e-10;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 NNTKRSIRIQGPGRFVTTIGKIG 24
 Db 1 NNTKRSIRIQGPGRFVTTIGKIG 24
 RESULT 7
 AAR38165
 ID AAR38165 standard; peptide; 24 AA.
 AC AAR38165;
 XX
 DT 27-AUG-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 12-OCT-1993 (first entry)
 XX
 DE V3 loop peptide N24G.
 XX
 KW gp120; HIV-1; cytotoxic T-lymphocyte; CTL; T-helper; AIDS; infection.
 XX
 OS Human immunodeficiency virus 1.

XX WO9310816-A1.
 XX
 PD 10-JUN-1993.
 XX
 PF 02-DEC-1992; 92WO-US010378.
 XX
 PR 02-DEC-1991; 91US-00800932.
 PR 16-SEP-1992; 92US-00945865.
 XX
 PA (PXA) UNIV TEXAS SYSTEM.
 XX
 PI Sastry JK, Arlinghaus RB, Platsoucas CD, Nehete PN;
 XX
 DR WPI; 1993-196739/24.
 XX
 PT Peptide composition for treating and preventing viral infections -
 PT comprise CTL-inducing epitope and HIV infection-inhibiting sequence or T
 PT helper cell-inducing sequence.
 XX
 PR Claim 19; Page 95; 130pp; English.
 PS
 CC HIV gp120 V3 loop-derived peptides (AAR38170-87) are successful in
 CC generating CTL responses, esp. peptide R15K (AAR38187); the T-helper cell
 CC -inducing peptide includes the sequence C19A (AAR38164); HIV infection-
 CC inhibiting peptides are given in AAR38188-206, and are esp. peptides
 CC R15K, N24G, E13V, R8K, T13Q and H13N (AAR38165-69). The peptides may also
 CC be derived from an influenza virus protein or a sendai virus protein
 CC (AAR41014-15). It was observed that peptide N24G (amino acids 308-311),
 CC with sequences derived from the V3 loop of HIV-1 IIIB, inhibits HIV-1
 CC infection of primary human T cells by 92% at 1 microg/ml (ca. 0.4-0.6
 CC micromol). (Updated on 25-MAR-2003 to correct PN field.) (Updated on 27-AUG
 CC -2003 to correct OS field.)
 XX
 SQ Sequence 24 AA;
 Query Match 100.0%; Score 122; DB 2; Length 24;
 Best Local Similarity 100.0%; Pred. No. 2.6e-10;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 NNTKRSIRIQGPGRFVTTIGKIG 24
 Db 1 NNTKRSIRIQGPGRFVTTIGKIG 24
 RESULT 8
 AAY22581
 ID AAY22581 standard; peptide; 24 AA.
 AC AAY22581;
 XX
 DT 17-OCT-2003 (revised)
 DT 19-OCT-1999 (first entry)
 XX
 DE HIV LDL binding peptide, sequence A.
 XX
 KW HIV; LDL; low density lipoprotein; human; immune response; infection;
 KW immunodeficiency; neoplastic tissue; myalgic encephalomyelitis; ME;
 KW viral infection fatigue syndrome; tuberculosis; hepatitis; AIDS; ARC;
 KW acquired immunodeficiency syndrome; AIDS related complex;
 KW HIV-infected CD4 cell; immunosuppressive peptide.
 XX
 OS Human immunodeficiency virus 1.
 XX
 PN WO9938524-A2.
 XX
 PD 05-AUG-1999.
 XX
 PF 28-JAN-1999; 99WO-IB000149.
 XX
 PR 29-JAN-1998; 98US-0072980P.
 XX
 PA (PREN/) PRENDERGAST P T.

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XX PI Prendergast PT;
XX DR WPI; 1999-494040/41.
XX XX
XX XX Enhancing the immune response using a recombinant human low-density
XX PT lipoprotein receptor, useful for treating viral infections, especially
XX PT human immunodeficiency virus (HIV) infection.
XX XX
XX PS Claim 7; Page 19; 24pp; English.
XX XX
XX XX This sequence represents a HIV sequence that binds human low density
XX CC lipoprotein (LDL), and is designated sequence "A". The invention relates
XX CC to a method for enhancing the immune response in a patient with a
XX CC condition, selected from immunodeficiency (due to a viral, bacterial,
XX CC mycoplasmic, fungal or parasitic infection, or from the growth of
XX CC neoplastic tissue), myalgic encephalomyelitis (ME), post inoculation or
XX CC viral infection fatigue syndrome, tuberculosis, or hepatitis. The method
XX CC comprises using a pharmaceutical composition, comprising a recombinant
XX CC human LDL receptor or a mimic molecule to the cysteine rich domain of LDL
XX CC receptor. The human recombinant LDL receptor forms pharmaceutical
XX CC compositions for: the treatment of acquired immunodeficiency syndrome
XX CC (AIDS) or ARC (AIDS related complex); reducing syncytium formation in HIV
XX CC -infected CD4 cells; treating blood or body fluid or organs to
XX CC neutralise/remove immunosuppressive peptides and/or viruses; or treating
XX CC hepatitis A, B or C. The pharmaceutical compositions also treat a viral
XX CC infection in a human or animal host. The human recombinant LDL receptor
XX CC is also useful for manufacturing medicaments for treating all the
XX CC conditions given above. The human recombinant LDL receptor is a highly
XX CC specific inhibitor of HIV-1 replication in vitro. (Updated on 17-OCT-2003
XX CC to standardise OS field)
XX SQ Sequence 24 AA;
    Query Match 100.0%; Score 122; DB 2; Length 24;
    Best Local Similarity 100.0%; Pred. No. 2.6e-10;
    Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NNTKRSIRIQRGPGRAFTVIGKIG 24
DB 1 NNTKRSIRIQRGPGRAFTVIGKIG 24
    |||||
RESULT 9
AAB15873
ID AAB15873 standard; peptide; 24 AA.
XX AC AAB15873;
XX DT 17-JAN-2001 (first entry)
XX DE Human chemokine derived peptide #25.
XX KW Macrophage recruitment; chemokine derivative; MCP-1; osteoporosis;
XX KW monocyte chemoattractant protein-1; inflammation; atherosclerosis; HIV;
XX KW AIDS; stroke; psoriasis; autoimmune disease; hypertension; endotoxaemia;
XX KW basophil-mediated disease; myocardial infarction; acute ischaemia;
XX KW rheumatoid arthritis; contraception.
XX OS Synthetic.
XX PN WO200042071-A2.
XX PD 20-JUL-2000.
XX PF 12-JAN-2000; 2000WO-US000821.
XX PR 12-JAN-1999; 99US-00229071.
XX PR 17-MAR-1999; 99US-00271192.
XX PR 01-DEC-1999; 99US-00452406.
XX PA (NEOR-) NEORX CORP.
XX XX

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PI Grainger DJ, Tatalick LM;
XX DR WPI; 2000-499101/44.
XX XX
XX XX New peptide 3, amide and heterocyclic compounds and saccharide conjugates
XX PT used for inhibiting chemokine induced activity and for treating e.g.
XX PT stroke, vascular diseases, autoimmune diseases and tumor growth.
XX PS Disclosure; Fig 18; 387pp; English.
XX XX
XX XX The present invention concerns the identification of a number of
XX CC chemokines which can be used to produce derivatives, agonists and
XX CC antagonists which are then useful in disease treatment. The chemokines
XX CC include sequences AAB15785-B15794, AAB15803-B15813 and AAB15831-B15848.
XX CC These chemokine derivatives can be used to treat diseases such as
XX CC autoimmune diseases, atherosclerosis, osteoporosis, HIV infection and
XX CC AIDS, psoriasis, inflammatory diseases, myocardial infarction, acute ischaemia and
XX CC rheumatoid arthritis, and can be used to prevent strokes and as
XX CC contraptives. The coding sequences for the chemokines can be used in
XX CC gene therapy for the same diseases, as well as in the production of
XX CC animal models.
XX SQ Sequence 24 AA;
    Query Match 100.0%; Score 122; DB 3; Length 24;
    Best Local Similarity 100.0%; Pred. No. 2.6e-10;
    Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NNTKRSIRIQRGPGRAFTVIGKIG 24
DB 1 NNTKRSIRIQRGPGRAFTVIGKIG 24
    |||||
RESULT 10
AAB68602
ID AAB68602 standard; peptide; 24 AA.
XX AC AAB68602;
XX DT 11-SEP-2003 (revised)
XX DT 25-APR-2001 (first entry)
XX XX
XX DE HIV gp120 V3 loop peptide #2.
XX KW HIV gp120 V3 loop; liposome composition; HIV infection.
XX OS Human immunodeficiency virus 1.
XX PN US6180134-B1.
XX PD 30-JAN-2001.
XX PF 07-JUN-1995; 95US-00480332.
XX PR 23-MAR-1993; 93US-00035443.
XX PR 29-SEP-1994; 94US-00316436.
XX PA (SEQU-) SEQUUS PHARM INC.
XX XX
XX PI Zalipsky S, Woodle MC, Martin FJ, Barenholz Y;
XX DR WPI; 2001-201897/20.
XX XX
XX PT Liposome composition for use in treating septic shock comprises liposomes
XX PT having an outer surface layer of polyethylene glycol chains, and a
XX PT polypeptide or polysaccharide effector molecule.
XX PS Disclosure; Fig 13; 32pp; English.
XX XX
XX CC The present invention relates to a liposome composition comprising
XX CC liposomes having an outer surface layer of polyethylene glycol chains,
XX CC each having a free distal end. A polypeptide or polysaccharide effector

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CC molecule is covalently attached to a portion of the distal ends. The
 CC effector interferes with specific binding of pathogen or cell in a
 CC bloodstream to a target cell or cell matrix, and is rapidly removed by
 CC renal clearance from the bloodstream when administered in free form. The
 CC liposome composition may be used in treating a condition mediated by
 CC binding a pathogen or cell in the bloodstream, to a target cell or cell
 CC matrix. It can be used in treating septic shock, toxic shock, colonic
 CC inflammation, leukaemic cell proliferation, or HIV infection. The present
 CC sequence is a peptide of the V3 loop of HIV envelope protein gp120. This
 CC peptide may be used in the composition of the present invention. gp120
 CC binds to the CD4 receptor during HIV infection of lymphocytes. By
 CC introducing the present peptide, the CD4 receptors are blocked, thereby
 CC inhibiting HIV infection. (Updated on 11-SEP-2003 to standardise OS
 CC field)

XX Sequence 24 AA;

Query Match 100.0%; Score 122; DB 4; Length 24;
 Best Local Similarity 100.0%; Pred. No. 2.6e-10;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNTKRSIRIQGPGRAFTVIGKIG 24
 |||||
 Db 1 NNTKRSIRIQGPGRAFTVIGKIG 24
 |||||

RESULT 1N

AAP90281
 ID AAP90281 standard; protein; 25 AA.

XX

AC AAP90281;

XX 09-SEP-2004 (revised)

DT 24-OCT-2003 (revised)

DT 25-MAR-2003 (revised)

DT 22-JUN-1990 (first entry)

XX Peptide 135 of HIV env gene.

XX HIV; AIDS; env gene; HIV vaccine; ds.

XX Simian-Human immunodeficiency virus.

OS Unidentified.

XX EP306219-A.

XX 08-MAR-1989.

XX 25-AUG-1988; 88EP-00307889.

XX 27-AUG-1987; 87US-00090080.

XX (REPK) REPLIGEN CORP.

XX Rusche JR, Putney SD, Jayaherian K, Farley J, Grimaila R, Lynn D;
 PI Petro J, Okeeffe T;

XX WPI; 1989-070387/10.

XX New HIV proteins and peptide(s) - used in diagnosis, prophylaxis or
 PT therapy of AIDS, esp. for prepn. of vaccines against HIV infection.

XX Claim 1; Page 27; 29pp; English.

XX Protein derivative stimulates a lymphocyte proliferative response in HIV-
 CC infected humans, providing a means of diagnosis, protection and
 CC therapeutic value. (Updated on 25-MAR-2003 to correct PR field.) (Updated
 CC on 25-MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to
 CC standardise OS field)

XX Revised record issued on 09-SEP-2004 : Correction to location

XX Sequence 25 AA;

Query Match 100.0%; Score 122; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 2.7e-10;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNTKRSIRIQGPGRAFTVIGKIG 24
 |||||
 Db 1 NNTKRSIRIQGPGRAFTVIGKIG 24
 |||||

RESULT 12

AAR08276
 ID AAR08276 standard; protein; 25 AA.

XX

AC AAR08276;

DT 07-MAR-1991 (first entry)

DE HIV peptide fragment (IIIB isolate).

XX AIDS; ARC; conjugate immunogen; Neisseria outer membrane protein;

KW HIV major neutralisation determinant.

XX Human immunodeficiency virus.

XX EP402088-A.

XX 12-DEC-1990.

XX 05-JUN-1990; 90EP-00306082.

XX 06-JUN-1989; 89US-00362176.

PR 06-JUN-1989; 89US-00362177.

PR 06-JUN-1989; 89US-00362178.

PR 06-JUN-1989; 89US-00362179.

XX (MERI) MERCK & CO INC.

XX Emini EA, Marburg S, Scolnick EM, Larson VM;
 WPI; 1990-370100/50.

XX Conjugate immunogen for AIDS and ARC treatment - composed of neutralising
 PT determinant of HIV and Neisseria outer membrane.

XX Claim 2; Page 22; 24pp; English.

XX This peptide is derived from the HIV IIIB isolate and is cross- reactive
 CC with the HIV major neutralisation determinant (MnD). This MnD is used
 CC in a conjugate, covalently linked to the outer membrane protein (Omp)
 CC from Neisseria, as an immunogen for vaccination against AIDS. A cocktail
 CC of different MnD poly- peptides can be used. See also AAR08274-75 and
 CC AAR08277

XX Sequence 25 AA;

Query Match 100.0%; Score 122; DB 2; Length 25;
 Best Local Similarity 100.0%; Pred. No. 2.7e-10;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNTKRSIRIQGPGRAFTVIGKIG 24
 |||||
 Db 1 NNTKRSIRIQGPGRAFTVIGKIG 24
 |||||

RESULT 13

AAR31276
 ID AAR31276 standard; peptide; 25 AA.

XX

AC AAR31276;

XX 12-FEB-1993 (first entry)

XX

DE	HIV principal determinant peptide.
XX	AIDS; ARC; human immunodeficiency virus; vaccine; Neisseria;
KW	meningitidis b; outer membrane protein complex; OMPC; PND135.
XW	Synthetic.
XX	
OS	
XX	
FH	Key Location/Qualifiers
FT	Modified-site 1
PT	/note= "bonds to the OMPC of the conjugate via this site"
XX	
PN	EP467700-A.
PD	22-JAN-1992.
XX	
PF	19-JUL-1991; 91EP-00306598.
XX	
PR	19-JUL-1990; 90US-00555339.
PR	19-JUL-1990; 90US-00555966.
PR	19-JUN-1991; 91US-00715276.
PR	19-JUN-1991; 91US-00715278.
XX	(MERI) MERCK & CO INC.
PA	
PI	Leanza WJ, Marburg S, Tolman RL, Emini EA;
DR	WPI; 1992-026505/04.
CC	Conjugate proteins comprising HIV peptide components - useful for preparing vaccines for e.g. AIDS or for treating infections.
PT	
XX	Claim 12; Page 56; 63pp; English.
PS	
XX	The invention relates to a co-conjugate comprising an immunogenic protein or protein complex having a first set of covalent linkages to low molecular weight moieties which have an anionic or polyanionic character at physiological pH, and a second set of covalent linkages to peptides comprising HIV principal neutralizing determinants (PND's) or immunologically equivalent peptides, preferably at least one set of the covalent linkages is comprised of maleimide derivatives; the (poly)anionic moiety is composed of one to five residues of the anionic form of a carboxylic, sulphonic or phosphonic acid; the immunogenic protein is the outer membrane protein complex (OMPC) of Neisseria meningitidis b; and the PND peptide has a linear structure, a disulphide-bonded cyclic structure, an amide-bonded cyclic structure or a thioether-bonded cyclic structure. The present sequence (PND135) is an example of a PND peptide component used in the co-conjugate. The co-conjugate is useful for inducing anti-peptide immune response in mammals, for inducing HIV-neutralizing antibodies in mammals, for formulating vaccines to prevent HIV infection or disease, including AIDS, or for treating humans afflicted with HIV infection or disease
XX	
SQ	Sequence 25 AA;
	Query Match 100.0%; Score 122; DB 2; Length 25;
	Best Local Similarity 100.0%; Pred. No. 2.7e-10; Indels 0; Gaps 0;
	Matches 24; Conservative 0; Mismatches 0;
QY	1 NNTKRSIRIQRGPGRAFTVIGKIG 24
DB	1 NNTKRSIRIQRGPGRAFTVIGKIG 24
	RESULT 14
ID	AAR30031 standard; peptide; 25 AA.
XX	
AC	AAR30031;
XX	
DT	25-MAR-2003 (revised)
DT	28-APR-1993 (first entry)
XX	
DE	HIV principle neutralising determinant 135.

XX	Human immunodeficiency virus; AIDS; PND; MIEP; conjugate; major immune enhancing protein; vaccine; anti-HIV antibodies; immunogen; passive immunisation.
XX	
OS	Human immunodeficiency virus.
XX	
PN	EP519554-A1.
XX	
PD	23-DEC-1992.
XX	
PF	11-JUN-1992; 92EP-00201693.
XX	
PR	19-JUN-1991; 91US-00715273.
XX	(MERI) MERCK & CO INC.
PA	
PI	Emini A, Liu MA, Marburg S, Tolman RL;
XX	WPI; 1992-425771/52.
DR	
XX	Conjugates of HIV-1 PND peptide(s) with the MIEP of Neisseria meningitidis - useful as a vaccine for treating and preventing HIV-1 infection, e.g. AIDS in humans.
PT	
PT	
XX	Claim 9; Page 59; 66pp; English.
PS	
XX	The peptide is HIV principle neutralising determinant (PND) 135 and is used as part of a conjugate comprising the major immune enhancing protein (MIEP) of Neisseria meningitidis covalently linked to the HIV PND. The conjugate may be used to prepare vaccines against HIV infections, e.g. AIDS, as research tools for studying PND structure-function relationships, or as immunogens for use in the passive immunisation of humans. (Updated on 25-MAR-2003 to correct PN field.)
CC	
XX	Sequence 25 AA;
SQ	
	Query Match 100.0%; Score 122; DB 2; Length 25;
	Best Local Similarity 100.0%; Pred. No. 2.7e-10; Indels 0; Gaps 0;
	Matches 24; Conservative 0; Mismatches 0;
QY	1 NNTKRSIRIQRGPGRAFTVIGKIG 24
DB	1 NNTKRSIRIQRGPGRAFTVIGKIG 24
	RESULT 15
ID	AAR26712 standard; peptide; 25 AA.
XX	
AC	AAR26712;
XX	
DT	09-FEB-1993 (first entry)
XX	
DE	HIV-PND-polysaccharide-protein conjugate vaccine.
XX	
KW	Human immunodeficiency virus; principal neutralizing determinant; outer membrane protein complex; OMPC; Neisseria; AIDS; PND135.
KW	
OS	Synthetic.
XX	
FH	Key Location/Qualifiers
FT	Modified-site 1..1
FT	/note= "Joins onto polysaccharide-protein complex via this site"
XX	
PN	EP468714-A.
XX	
PD	29-JAN-1992.
XX	
PF	19-JUL-1990; 90US-00555558.
XX	
PR	19-JUL-1990; 90US-00555558.


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PR 19-JUL-1990; 90US-00555974.
PR 19-JUN-1991; 91US-00715275.
PR 19-JUN-1991; 91US-00715277.
XX
XX (MERI ) MERCK & CO INC.
XX
XX Marburg S, Tolman RL, Emini EA;
XX
XX WPI; 1992-034437/05.
XX
XX HIV peptide-polyaccharide-protein conjugates - used in vaccines or to
XX produce antibodies to prevent or treat HIV infection.
XX
XX Claim 9; Page 57; 63pp; English.
XX
XX The invention relates to a conjugate of an HIV principal neutralizing
XX determinant (PND), or an immunologically equivalent peptide (PEP),
XX covalently coupled to an immunogenic protein or protein complex through
XX an anionic polyaccharide linker. Pref. the immunogenic protein is the
XX outer membrane protein complex (OMPC) of Neisseria meningitidis b and the
XX PND peptide has a linear structure, a disulphide-bonded cyclic structure,
XX an amide-bonded cyclic structure or a thioether-bonded cyclic structure.
XX The present sequence (PND135) is an example of a PND peptide component.
XX The conjugates are used for inducing HIV-neutralising antibodies or for
XX making vaccines to prevent contraction of HIV infection or disease. The
XX antibodies can be used for passively protecting against infection by HIV,
XX or for protecting against proliferation of HIV post-infection, or for
XX treating AIDS, or in diagnostic assays
XX
XX SQ Sequence 25 AA;
XX
XX Query Match 100.0%; Score 122; DB 2; Length 25;
XX Best Local Similarity 100.0%; Pred. No. 2.7e-10;
XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 NNRKSIRIQRGPGRAFTVIGKIG 24
XX |||||
XX Db 1 NNRKSIRIQRGPGRAFTVIGKIG 24
XX
XX Search completed: June 3, 2005, 03:17:35
XX Job time : 165 secs

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